

PS	Disclosure; Page 31-33; 51pp; English.	
CC	This sequence encodes the rat serotonin St-B173 receptor and was encoded by the clone St-B173. The putative intron, found in clone St-B172, was absent from this clone with the flanking exons being spliced together at nucleotide 873. Splicing at this position results in a 131 bp open reading frame encoding a protein of 437 amino acids with a molecular weight of 46.8 kD. Hydrophyt analysis of this amino acid sequence indicated several hydrophobic regions predicted to represent putative transmembrane spanning domains. When compared to previously cloned G-protein coupled receptors, the transmembrane regions of St-B17 exhibited high homology to various serotonin (5-HT) receptors suggesting that it may be a member of this receptor family. Within the transmembrane regions, St-B173, exhibits homology of 41%, 39%, 38% and 36% with 5-HM2, 5-HM1C, 5-HT1B, 5-HT1A and 5-HT1E receptors respectively. The isolated gene, St-B17, encodes a protein which may be used to test CNS activity of drug candidates.	
XX	Sequence 437 AA;	
QY	Query Match 82.6%; Score 1893.5; DB 14; Length 437; Best Local Similarity 84.3%; Pred. No: 8.2e-176; Matches 375; Conservative 11; Mismatches 46; Indels 13; Gaps 0	
DB	1 MVEPEPGPTANSTPAWGGGPPSAPGGSGWVAALCVVIALTAANSLLIACTOPALRENT 60 1 mypepppnspstapwppgppppggsgwaaalcvvilaapsllivlctqavnt 60	
QY	61 SNFFLYSLIFTSQMLVGUVMPAMPMLNLYGRRAWLARGICLILWTAQDFYMCASATILNLCLLI 120 61 snffivsiftsdlmvguvmpampmlnlygrwlvargclwltafdvncasailncli 120	
DB	121 SLDRYLILSPRYKLMNTPLALAVLGAWLAALASFLPLLGWHLGHARPPVCGQC 180 121 sdrylilsprykilmntplalavlgawlaalasflpllgwhlgharppvcqc 180	
QY	181 RILASUPFLVYASGLTFFLPSGAICFYCRILLAARKAQWAQLSLITGMASOSETQV 240 181 rillasupflvylasgvttflpsgaicfycrillaarkaqwasylttgtagalletiqvp 240	
DB	241 RTPRPGVESADSRRRLATRHSRALKAKMLGILGMMFVTWLPFFVANIVQAVCDCTS PG 300 241 rtprgmesadsrrrlatrkhsrkalkastlg119mfvtwlpffvaniaqvacdcts pg 300	
QY	301 LFDVLUWLGIGCNSTMNITYPFMRDKRKGRLPFCPRCPBPEROASLAPS-----RT 355 301 lfdvluwlgicnstmnitypfmrdkrkgrlpfcprcpbperoaslaps-----rt 355	
DB	356 SHSGPRGLSLOQVLPLRPPSDSDSAGSGSSGLRULAQOLPCEBATQDPLPRAA 415 357 qrcqtrp--qqqlvalipppsdas--asqgtsgjqqltaqdilgeatrdppprat 412	
OY	416 AAVNNFFNDPAPPELRLRPHPLGIFTN 440 413 tvvnfftdsveipeirphplspyn 437	
RESULT	2	
ID	ABB70765 standard; Protein: 477 AA.	
XX		
AC	ABB70765;	
DT	18-MAY-2001 (first entry)	
DE	Human betal-adrenoreceptor protein.	
KW	Betal-adrenoreceptor; human; mutation; disease predisposition; cardiomyopathy; dilative.	
XX		

WO200111039-A2.
Homo sapiens.
15-FEB-2001.
04-AUG-2000; 2000WO-DE02648.
05-AUG-1999; 99DE-1038390.
(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
Wallukat, G., Podlowski, S., Wenzel, K., Mueller, J.;
WPI; 2001-202770/20.
New mutated gene for human betal-adrenoreceptor, useful for drug development and in genotyping for predisposition to cardiomyopathy
Claim 4; Page 22-23; 23pp; German.

Db	386 afqrlccaraacrr-----raah-gdrprasgclaragpppspgaaasddd 433	CC	e.g. diabetes. The canine version of RA-Ca-b3 can be used to develop treatments specific for dogs. The sequence can also be used in differential screening for ligands for RA-Ca-b3 as compared to the beta-2 adrenergic receptor (AAW4932).
Qy	384 AGSGSSGIRL 394	CC	
Db	434 dvvgatpparl 444	CC	
SQ	Sequence 405 AA;	XX	
RESULT	3	Query Match	24.4%; Score 558.5; DB 19; Length 405;
ID	AAW4933 standard; protein; 405 AA.	Best Local Similarity	35.6%; Pred. No. 6.5e-46;
XX		Matches	148; Conservative 59; Mismatches 154; Index 55; Gaps 15;
AC	AAW4933;	Db	18 ptptpdant---sglpgapawavalagalaalelatvqgnlvivaiartptqlgtm 73
XX		QY	63 FFLVLSIFTSIDLNGLVUMPRAMNLAYGRVNLARGVLARGCLCLIAFDVMCCSASILNCLISI 122
DE	Canine beta-3 adrenergic receptor.	Db	74 vftvtslatadavvgilvvppgataltgrplgatgcelsvwsvdvcvtasietcalav 133
XX		QY	123 DRYLLILSPKRYKLMTPLRLALVIGAWLAASFLPLIGLWHLG-----HARPE 174
KW	hybridisation; ligand; ss.	Db	134 dylavtnpnyrgalvtkraraavvluwvysaavsfapinskwvrvyadadeaqchsnop 193
XX	Canis familiaris.	FT	26..28 /note= "Asn is N-glycosylated"
PH	Key Modified-site Location/Qualifiers	FT	38..63 /note= "Asn is N-glycosylated"
FT	Modified-site	FT	76..99 /label= transmembrane domain 1
FT	Domain	FT	110..131 /label= transmembrane domain 2
FT	Domain	FT	156..178 /label= transmembrane domain 3
FT	Domain	FT	203..226 /label= transmembrane domain 4
FT	Domain	FT	293..314 /label= transmembrane domain 5
FT	Domain	FT	322..347 /label= transmembrane domain 6
FT	Domain	FT	/label= transmembrane domain 7
PN	W09735973-A2.	RESULT	4
XX		ID	AAR32501
PD	02-OCT-1997.	XX	AAR32501 standard; protein; 400 AA.
XX		AC	AAR32501;
PF	26-MAR-1997; 97WO-FR00537.	XX	
XX		DT	09-JUN-1993 (first entry)
PR	26-MAR-1996; 96FR-0003730.	XX	
RR	(VETI-) VETIGEN.	DE	Beta-adrenergic receptor.
XX		KW	Fat cell specific; BAR; lipolysis; obesity; diagnosis;
PI	XX	XX	OS Rattus rattus.
DR	WPI: 1998-032136/03.	XX	Rattus rattus.
DR	N-PSDB; AAV30469.	PN	US7783602-A.
XX		PD	15-DEC-1992.
PT	Canine beta 2 and beta 3 adrenergic receptors and coding sequences - useful for identifying specific ligands and (ant)agonists to develop specific treatments for obesity in dogs	XX	11-NOV-1991; 91US-0783602.
PT	XX	PR	01-NOV-1991; 91US-0783602.
PS	Claim 3; Page 54-55; 79pp; French.	XX	
PS	WPI: 1998-032136/03.	PA	(USSH) US DEPT HEALTH & HUMAN SERVICE.
CC	This sequence represent the canine beta 3-adrenergic receptor	XX	Venter CJ;
CC	(RA-Ca-b3). The coding sequence was isolated from a cDNA library constructed from polyA+ RNA purified from dog brown adipose tissue cells.	XX	WPI; 1993-067426/08.
CC	The probe was a fragment of the coding region of the human beta-3 adrenergic receptor covering the region from the initiation codon to the transmembrane domain 7 (Tm7) amplified by primers AAV30511-V30512. The full length insert was cloned into M13 for sequencing using primers AAV30470-V30490. The sequence can then be expressed e.g. in a mammalian cell, by subcloning into an expression vector such as pCDNA3. RA-Ca-b3 has been implicated in obesity and obesity-related metabolic disorders	XX	Fat cell specific beta- adrenergic receptor polypeptide - used for diagnosis of obesity due to inactive lipolysis

QY 235 ETIQVPRTRPGVESADSR-----RLATKHSRALKAKLKLIGLIGFETVWLPFFVA 287
 DE | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
 Db 247 epspspgprpadslangsskrpsrivalreqkalk---tigimyfticwipffla 303.
 QY 288 NTIQAV-CDCISPGFLFDVTLWLGICNSTMNPIV--PLFMRDFKRALGRFLPCCR--C 340
 DE | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
 Db 304 nvrkafhndlvpdlfvfwnlyjansanaplycrsp---dfkafarlccarrac 359
 QY 341 PR 342
 DE Db 360 rr 361

RESULT 8
 AAR54992 standard; Protein; 400 AA.
 XX AAR54992;
 XX 23-JAN-1995 (first entry)
 DE Murine beta-3 adrenergic receptor.
 XX KW Receptor; beta; adrenergic; testing; screening; identification;
 KW drugs; adenylate cyclase; hormone; lipase; signal transduction.
 XX OS Mus musculus.
 XX PN EP600136-A.
 XX PD 08-JUN-1994.
 XX PF 01-DEC-1992; 92EP-0403248.
 XX PR 01-DEC-1992; 92EP-0403248.
 XX PA (CNRS) CENT NAT RECH SCI.
 PI Emirine L, Nahmias-kaminski C, Strosberg AD;
 DR WPI: 1994-177542/22.
 DR N-FSSDB; AAQ65477.
 XX PT Isolated and purified polypeptides having beta3-adrenergic
 PT receptor activity - are used to study the effects of various
 PT chemical agents on the beta3-adrenergic receptor.
 XX
 CC The coding sequence of the beta-three adrenergic receptor can be
 CC used in expression vectors which are then used to transform cells.
 CC The cells then express the receptor on their surfaces and can be
 CC used to study the effects of various chemical agents on the receptor
 CC which is coupled to adenylate cyclase and hormone sensitive lipases.
 XX SQ Sequence 400 AA;

Query Match 24.1%; Score 552.5; DB 15; Length 400;
 Best Local Similarity 35.1%; Pred. No. 2.4e-45; Mismatches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

QY 5 PGPIANSTPA-WGACP--PSAPGCG---WVARACWIAL-TAANSLLRATICQ 54
 DE 3 pwpngrstalwsdaptidpsaantsgipgpwaaalalaataygnlvniaart 62
 QY 55 PAIIRNTSNFLVLFSRFTSDIMGLVMPAMLNAYGRWILARGLCLWTFDVMCCSASI 114
 DE 63 prlqitlnvfvtslaadivvg1lmpptatlgtwhplgetcclwsvdvicvtas 122
 QY 115 LNCLLISDRYLILSPRLRYKLRTPRLALVIGAWSLAALASPLPLIGWELG--- 170

RESULT 9
 AAR15498 standard; Protein; 446 AA.
 XX ID AAR15498;
 XX AC AAR15498;
 XX DT 08-MAR-1992 (first entry)
 DE Human dopamine D1 receptor.
 XX KW catecholamine; G-protein-coupled receptor; neurotransmitter;
 KW adenyllyl cyclase stimulation.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 PR FT Modified-site 5
 PA FT /label= OTHER
 FT FT /note= "N-glycosylation site - putative"
 FT FT /label= transmembrane
 FT FT /note= "I"
 FT FT Domain 175
 FT FT /label= OTHER
 FT FT /note= "N-glycosylation site - putative"
 FT FT /label= transmembrane
 FT FT /note= "II"
 FT FT Domain 23..49
 FT FT /label= transmembrane
 FT FT /note= "III"
 FT FT Domain 62..87
 FT FT /label= transmembrane
 FT FT /note= "II"
 FT FT Domain 94..120
 FT FT /label= transmembrane
 FT FT /note= "III"
 FT FT Domain 138..164
 FT FT /label= transmembrane
 FT FT /note= "IV"
 FT FT Domain 192..218
 FT FT /label= transmembrane
 FT FT /note= "V"
 FT FT Domain 273..299
 FT FT /label= transmembrane
 FT FT /note= "VI"
 FT FT Domain 311..337
 FT FT /label= transmembrane
 FT FT /note= "VII"
 FT Region 265..268
 FT FT /label= Protein_kinase_A_phosphorylation_site
 FT FT /note= "putative"
 FT Region 338..343
 FT FT /label= Protein_kinase_A_phosphorylation_site
 FT FT /note= "putative"
 DE Db 356 l1csyygrgpeepiavtfpaspvearqspplnrfddyegarp 397

QY 171 ---HARPPVGQCRLLASLPFVLVLAASGLTFLFLPSGACITFCYCRLLAARKQAVQASLT 226
 DE Db 183 aqechnsprc---csfasnmpyalissvsvfypl1vmlfyavarvrvakqr-hlire 238.
 QY 227 TGMASQASSETLQVPRPRP-----GESADSR--RLATKHSRALKAKLKLIGL 274
 DE Db 239 1grfsspeepspsrspspatgtapaadgvppcgrrparilplrehral---tigim 295
 QY 275 GMFFVTWLPPFWVANIQAVC--DCISPLGFDFLTLWLGICNSTMNPIV--PLFMRDFKR 329
 DE Db 296 9ifslcwlpfflanviralagapslpsgvfialnwqyansafnpvycrsdpdrafr 355

QY 330 AL---GRFLPCPRC--PREROASLASPLSR-TSHSGPRP 352
 DE Db 356 l1csyygrgpeepiavtfpaspvearqspplnrfddyegarp 397

QY 123 etccalavdry-lavtoplyrgiltvkrraraawvliwivsaafajmsqwwrgadae 1822
 DE Db 171 ---HARPPVGQCRLLASLPFVLVLAASGLTFLFLPSGACITFCYCRLLAARKQAVQASLT 226
 DE Db 183 aqechnsprc---csfasnmpyalissvsvfypl1vmlfyavarvrvakqr-hlire 238.
 QY 227 TGMASQASSETLQVPRPRP-----GESADSR--RLATKHSRALKAKLKLIGL 274
 DE Db 239 1grfsspeepspsrspspatgtapaadgvppcgrrparilplrehral---tigim 295
 QY 275 GMFFVTWLPPFWVANIQAVC--DCISPLGFDFLTLWLGICNSTMNPIV--PLFMRDFKR 329
 DE Db 296 9ifslcwlpfflanviralagapslpsgvfialnwqyansafnpvycrsdpdrafr 355

QY 330 AL---GRFLPCPRC--PREROASLASPLSR-TSHSGPRP 352
 DE Db 356 l1csyygrgpeepiavtfpaspvearqspplnrfddyegarp 397

XX 28-NOV-1991.

XX	13-MAY-1991;	91W0-US03308.	XX	AC AAR38364;
PR	17-SEP-1990;	90US-0523237.	XX	AC AAR38364;
PR	14-MAY-1990;	90US-0523237.	XX	AC AAR38364;
XX	17-AUG-1994 (first entry)		XX	AC AAR38364;
PA	(UVDU-) DUKE UNIV.		XX	AC AAR38364;
PA	(UVOR-) OREGON HEALTH SCI UNIV.		XX	AC AAR38364;
XX	Bunzow JR, Civelli O, Grandy DK, Zhou OY, Caron MG;		KW Dopamine D1 receptor; adenylylate cyclase stimulation;	
PI	Dearry A, Falardeau P, Gingrich JA;		KW cAMP-dependent protein kinase activation; psychomotor disorders;	
XX	WPI: 1991-369177/50.		KW intronless gene; G-linked receptor family; neuron growth; neuron differentiation.	
DR	N-PSDB; AAQ44954.		XX	DE Human dopamine D1 receptor.
XX	Cloned gene encoding Di-dopamine receptor - useful for e.g. drug screening, diagnosis of e.g. Parkinson's disease or schizophrenia or in gene therapy		XX	DE Human dopamine D1 receptor.
PT			XX	DE Human dopamine D1 receptor.
PT			XX	DE Human dopamine D1 receptor.
XX	Example 1: Fig 1B; 52bp; English.		XX	DE Human dopamine D1 receptor.
PS			XX	DE Human dopamine D1 receptor.
XX	The D1 dopamine receptor sequence was obtained from two overlapping clones, one genomic (HG126) and the other from a human retina cDNA library (D233). The amino acid sequence was deduced from the nucleotide coding sequence. The receptor is similar to known G-protein coupled proteins, e.g. Cys351) in the carboxyl terminus near transmembrane VII is conserved in most G-protein-coupled receptors; it may be palmitoylated. The carboxyl tail also contains several putative sites for phosphorylation by an agonist-dependent receptor kinase.		XX	DE Human dopamine D1 receptor.
SQ	Sequence 446 AA:		XX	DE Human dopamine D1 receptor.
	' Query Match 24.1%; Score 552.5; DB 12; Length 446; Best Local Similarity 31.2%; Pred. No. 2.8e-45; Matches 143; Conservative 79; Mismatches 172; Indels 65; Gaps 13;		XX	DE Human dopamine D1 receptor.
CC	21 SARGGSGW-----AAALCWLTAANSLILALICTOPALRN-TSNFLVSL 68		CC	CC was isolated from a lambda EMBL3 SP6/77 human genomic library. The library was probed by a known 450bp rat D1 clone. Three positive clones with inserts of ca. 14kb were isolated. One of the clones was restriction analysed and sequenced to reveal an open reading frame of 1476 bp encoding a 446 amino acid protein.
CC	7 sandgtglverdfsrltaclflsllstlgtlncaavirfrhlrskvtnffvsl 66		CC	CC The D1 receptor belongs to the G-protein family; it regulates neuron growth and differentiation, influences behaviour and modifies D2 receptor-mediated events.
CC	69 FTSIDLMLGVVMPAMNLALYGRWVLARGCLULWTADVMCCSASTUNCLISDRYLLI 128		CC	CC
CC	67 avsdllavlvmpkavaeiagtwpfq-sfcniiwafdimcstasinlcvsvdrywai 125		CC	CC
CC	129 LSPRLRYKIRMLPRLALVALGAWSLAALASFLPLLGWHELGHARPPVFG----- 178		CC	CC
CC	126 sspryerkmtpkaaflisavwtlsvlswtfsipyqlswhk--akptspsgnatslaet 182		CC	CC
CC	179 -OCLRLLASLPVFLVAGLTFPFFGATTCRILAAKRQAVOVAL-TTGMASOAE 235		CC	CC
CC	183 idodsslsrttyaisssvisfypvaimivtytriyraqkqirriaaleraavhaknq 242		CC	CC
CC	236 TIQVPRTPRGVESADRRRLAKHRSRKALKLTGIGMFTWVLPFFVANIQVCD 295		CC	CC
CC	243 tt-tgngkpvccspessfkmstkrktvkl---tisvingvfvccwipffincilpcg 299		CC	CC
CC	296 -----CISPGLEDFVLTWLGLCNCSTMMPPIYIPLFMRDFKRALGRFLPCPR-CPREROA- 346		CC	CC
Db	300 sgetqpcidnsntfdvfwfgwansinply-afnedfrkfstlqcyrlcpatmna 358		Db	7 sandgtglverdfsrltaclflsllstlgtlncaavirfrhlrskvtnffvsl 66
Qy	347 -----SLASPLSLTSHSGSRPGISLQQVLPPLPBDSDSDSGSSGLRLTAQQLP 401		Qy	69 FTSIDLMLGVVMPAMNLALYGRWVLARGCLULWTADVMCCSASTUNCLISDRYLLI 128
Db	359 etrsinmngaaftsshneprgsiskecnlyiiphavgssedikkeeagiarpleklsp 418		Db	67 avsdllavlvmpkavaeiagtwpfq-sfcniiwafdimcstasinlcvsvdrywai 125
Qy	402 GEATODPUPTRAAAVNPFENITOPAEPPLP-----HP 434		Qy	129 LSPRLRYKIRMLPRLALVALGAWSLAALASFLPLLGWHELGHARPPVFG----- 178
Db	419 -----alsvildydatvslekiqptlqngqhp 445		Db	126 sspryerkmtpkaaflisavwtlsvlswtfsipyqlswhk--akptspsgnatslaet 182
Qy	236 TIQVPRTPRGVESADRSRLLAKHRSRKALKLTGIGMFTWVLPFFVANIQVCD 295		Qy	179 -OCLRLLASLPVFLVAGLTFPFFGATTCRILAAKRQAVOVAL-TTGMASOAE 235
Db	243 tt-tgngkpvccspessfkmstkrktvkl---tisvingvfvccwipffincilpcg 299		Db	183 idodsslsrttyaisssvisfypvaimivtytriyraqkqirriaaleraavhaknq 242
Qy	296 -----CISPGLEDFVLTWLGLCNCSTMMPPIYIPLFMRDFKRALGRFLPCPR-CPREROA- 346		Qy	236 TIQVPRTPRGVESADRSRLLAKHRSRKALKLTGIGMFTWVLPFFVANIQVCD 295

Best Local Similarity 35.9%; Pred: No. 1e-44; Matches 139; Conservative 59; Mismatches 137; Indels 52; Gaps 16;

Db 300 sgetqpfcdsntdfvfwfgwansslnpilyafnadrkfakstlgcycrpataai 358
QY 347 ---SLASPSLRTSHSPRGPLSQQVLPPLPPDSDPSDPAAGGGSGIRITAQLLP 401
Db 359 etysvinnangaaamishheprgsksikcvyliphavgsedikkkeeaaagirplekisp 418
QY 402 GEATQDPPLPTRAANAVNFFNIDAEPEELRP---HP 434
Db 419 -----alsvildydtaslekiqpitqngqhp 445

RESULT 11
RAR25698 ID AAR25698 standard; Protein: 388 AA.
XX AC AAR25698;
XX SQ 20-JAN-1993 (first entry)

Murine adrenergic beta-3 receptor.

XX KW Mouse; Polymerase chain reaction; transmembrane region; adrenergic receptor.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Domain 35..60
FT Domain /label= transmembrane
FT Domain 70..97
FT Domain 110..129
FT Domain 153..175
FT Domain /label= transmembrane
FT Domain 201..222
FT Domain 290..311
FT Domain /label= transmembrane
FT Domain 324..344
FT Domain /label= transmembrane
PN WO9212246-A.
XX PD 23-JUL-1992.

XX PR 14-JAN-1991; 91FR-0000320.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Emorine LJ, Nahmias C, Strosberg AD;
XX DR WPI: 1992-268668/32.
DR N-PSDB; RQ26808.

XX PT Murine adrenergic beta-3-receptor and nucleic acid encoding it - for treating diabetes, obesity and hyperlipidaemia, and also for identifying ligands with beta-3 affinity
XX PS Claim 13; Page 37; 61pp; French.

The murine beta-3 adrenergic receptor gene encodes a polypeptide with 82% homology with the human beta-3 adrenergic receptor. The homology is concentrated in the 7 transmembrane domains. See also AAO26804-7.

XX Sequence 388 AA;

Db 115 LNCLCLISUDRYYLTLSPRLKRMTPKLALALVGLGANSALASFLPULLGRHELG---
Db 123 eticalalavdrylavltnplrygtlvtktraraavavlwivsaavsfapimswqrvgadae 182
QY 171 ---HARIPVPGCOCRLASLPEVILVASSGLTTEFLPSGAICFTYCIRILAAARKAVOASLT 226
Db 183 aeqchsnprcc--csfaasnmpyalisssvstpyplvnmlfvawrvfavrkar-hlrr 238
QY 227 TGMASQASETLLQVPRTPR-----GVESADSR--RLATKHSRKALKAKLTGILL 274
Db 239 1gftspeespsspsrspspatggtpaadpgvpcgprparilpribralr---tiglim 295
QY 275 GMFVTWLFVFVANIQAVC--DCISPGLFDVITWLGCNCSTMNPILY--PLFMRDFKR 329
Db 296 gitslcwlpfflanvlralagpslvpsgvfialnwqgyansafnpvycrsp---dfrd 351
QY 330 ALGRFLPQP--RCPREQASL--ASP 351
Db 352 afrrll-csyggcggpeeprrtfasp 377

RESULT 12
ID AAW09795
XX AC AAW09795;
XX DT 11-JUN-1997 (first entry)
XX DE D1 dopamine receptor.
XX OS Rattus rattus.
XX FH Key Location/Qualifiers
FT Modified-site 45
FT /note= "N-linked glycosylation site"
PN US5610282-A.
XX PD 11-MAR-1997.
XX PF 06-JUL-1990; 900S-0548714.
PR 06-JUL-1990; 900S-0548714.
PR 11-MAR-1993; 930S-0029917.
PR 19-MAY-1995; 950S-0444734.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Mahan LC, Movittie LD, Monsma FJ, Sibley DR;
XX DR WPI; 1997-178452/16.
XX N-PSDB; AAT63657.
XX PT DNA encoding D1 dopamine receptor protein - for production of
PT transfecting cells used for drug screening
XX PS Claim 1; Column 11-16; 24pp; English.

XX
CC
CC
CC
CC
CC
XX
SQ

The sequence is the rat D1 dopamine receptor protein which is linked to the activation of adenylyl cyclase activity. The receptor also couples with guanine nucleotide binding regulatory (G) proteins. By constructing cell lines that express the D1 receptor, the affinities and efficacies of agonist and antagonist drugs can be assessed.

Sequence 487 AA;

Query Match 23.3%; Score 533.5; DB 18; Length 487;
Best Local Similarity 33.3%; Pred. No. 2.2e-43; PA
Matches 134; Conservative 72; Mismatches 157; Indels 39; Gaps 12;

OY 30 AAALCIVVIALTAANNSLLAALICTOPALRN-TSNFLFLSFTSDLMVGIVWMPAMLN 88
Db 67 acfslislistlgtlniyraqkqirraleraavhakncttagngnpvecaqsssfk 126

OY 89 YGRWLARGLCLWTAFDVMCCSASILNCLSIDRYVILSLPLRYKLRMTPRLALAVL 148
Db 127 agfwplg-pfcniwafdmctaslinlvicvsvdrywaisspfgyerkmtpkaafii 185

OY 149 GAWSLAALASFPLPILLGWHELGHARP-PVPG-----QCRLLASLPVLVAGL 195
Db 186 vafitlsvifspqswik--akptwpldnftslededndctrslrtvaissli 242

OY 196 TFFLPSGAICFTYCIRILLAARKQAVQSL-TMGMASQASETIVQVPRPRPGYESADRR 254
Db 243 slypvaimivtyrsyriaqkqirraleraavhakncttagngnpvecaqsssfk 302

OY 255 LATKHSRKAKAKTIGLGMFVTWIPFFVANTIQAVCD-----CISPLFDVLTW 307
Db 303 msfkretkvl--tisvingvfvccwlpffisnmvpfcgseetqpcidsitfdvfw 359

OY 308 LGICNSTMMPILIPFLMRDFKRAIGRFLPCPR-CPREROASIASPSLR-----TSHSG 359
Db 360 fgwanssinpiy-afnadfqkafstilgcyricpttna-letsvisnnngavvffshtie 417

OY 360 PRPGLSLQQWLPLPLPPDSDSDAGSGSSGSRITAQLLP 401
Db 418 prgsiskdcnlvyliphavgsseelkkkeeaggiakpleklsp 459

RESULT 13
AARI5499
ID AARI5499 standard; Protein; 446 AA.
AC AARI5499;
DE Rat dopamine D1 receptor.
XX Rattus rattus.

Key Modified-site Location/Qualifiers
FT Modified-site 4 /label= OTHER
FT /note= "N-9-Gycosylation site - putative"
FT Modified-site 174 /label= OTHER
FT /note= "N-9-Gycosylation site - putative"
FT Modified-site 135 /label= protein_kinase_A_phosphorylation_site
FT /note= "putative"
FT Modified-site 229 /label= "Protein_kinase_A_phosphorylation_site
FT Modified-site 268 /label= Protein_kinase_A_phosphorylation_site

/note= "putative"

FT XX
PN WO9118005-A.
XX PD 28-Nov-1991.
XX PF 13-MAY-1991;
PA (UYOR-) DUKE UNIV.
PA (UYOR-) OREGON HEALTH SCI UNIV.

XX PI Bunzow JR, Civelli O, Grandy DK, Zhou OY, Caron MG;
PI Dearry A, Falardeau P, Gingrich JA;
XX DR N-PSDB; AAQ14955.

XX PT WPI; 1991-36917/50.
PT Cloned gene encoding D1-dopamine receptor - useful for e.g. drug screening, diagnosis of e.g. Parkinson's disease or schizophrenia or in gene therapy

XX PS Example 9; Fig 3A; 52pp; English.

XX The D1 dopamine receptor sequence was obtained from two overlapping clones, one genomic and the other from a rat striatum cDNA library. The amino acid sequence was deduced from the nucleotide coding sequence. The receptor is similar to the human D1 dopamine receptor (see AARI5498) and known G-protein coupled proteins, e.g. Cys(351) in the carboxyl terminus is conserved in most G-protein coupled receptors; it may be palmitoylated. The carboxyl tail also contains several putative sites for phosphorylation by an agonist-dependent receptor kinase.

XX SQ Sequence 446 AA;

Query Match 23.2%; Score 531.5; DB 12; Length 446;
Best Local Similarity 33.1%; Pred. No. 3.1e-43; PA
Matches 133; Conservative 72; Mismatches 158; Indels 39; Gaps 12;

OY 30 AAALCIVVIALTAANNSLLAALICTOPALRN-TSNFLFLSFTSDLMVGIVWMPAMLN 88
Db 26 acfslislistlgtlniyraqkqirraleraavhakncttagngnpvecaqsssfk 85

OY 89 YGRWLARGLCLWTAFDVMCCSASILNCLSIDRYVILSLPLRYKLRMTPRLALAVL 148
Db 144 agfwplg-pfcniwafdmctaslinlvicvsvdrywaisspfgyerkmtpkaafii 261

OY 149 GAWSLAALASFPLPILLGWHELGHARP-PVPG-----QCRLLASLPVLVAGL 195
Db 145 vafitlsvifspqswik--akptwpldnftslededndctrslrtvaissli 201

OY 196 TFFLPSGAICFTYCIRILLAARKQAVQSL-TMGMASQASETIVQVPRPRPGYESADRR 254
Db 202 slypvaimivtyrsyriaqkqirraleraavhakncttagngnpvecaqsssfk 318

OY 255 LATKHSRKAKAKTIGLGMFVTWIPFFVANTIQAVCD-----CISPLFDVLTW 307
Db 262 msfkretkvl--tisvingvfvccwlpffisnmvpfcgseetqpcidsitfdvfw 359

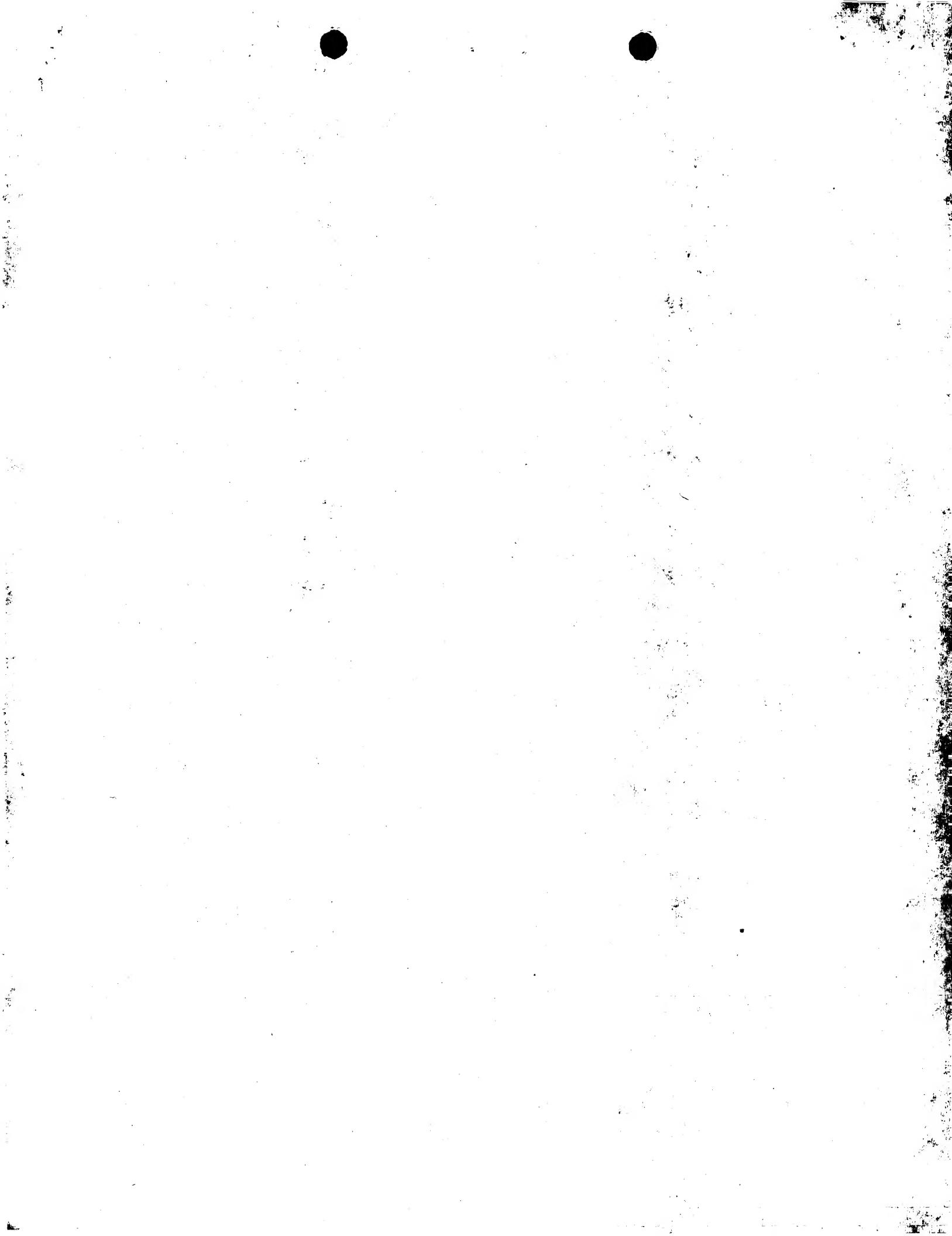
OY 308 LGICNSTMMPILIPFLMRDFKRAIGRFLPCPR-CPREROASIASPSLR-----TSHSG 359
Db 319 fgwanssinpiy-afnadfqkafstilgcyricpttna-letsvisnnngavvffshtie 376

OY 360 PRPGLSLQQWLPLPLPPDSDSDAGSGSSGSRITAQLLP 401
Db 377 prgsiskdcnlvyliphavgsseelkkkeeaggiakpleklsp 418

RESULT 14

Db 70 mtnvrvtslaadlvingllvvppaatlatghwpligatgcelwtsvdvcvtaستica 129
 Qy 120 ISLDRVLLISPLRYKLRMTPRLALVLAGWSLAALASFLPULLGWHLG-----H 171
 Db 130 lavdrylavtgvrlqyalgvtkrcartavlywvsaafsapimsqwvrgadaeqrch 189
 Qy 172 ARPPVGQCRILASLPFLVKGTLPSGAICFTYCRILLAAKQAVQASLTGMS 231
 Db 190 snprc--cafasmnpvylssvsvstlyplvmlfyarfvvatcq--lrllrgelg 242
 Qy 232 Q--ASETLOVER-----TPRGVEGADSR--RLATKHSRALKAKLTGIGLM 276
 Db 243 rfppeesppapsrslapavpgtcappgvpacgrparlpirehral--ctglingt 299
 Qy 277 FFVUTWMPFFVANIQVQ-COCISPG-LFDVLTWLGCONSTANTPIY--PLEMDIKRA 331
 Db 300 fticwlpffianviralggpsilvpapflainwlyanzansainplicyrsdpfsafrll 359
 Qy 332 --GRRLPCRCPRERQASL--PSLRTSHSISGR 361
 360 crcgrllrppecaarpalpfsgvpaarspaqr 394

Search completed: March 15, 2002, 14:11:21
Job time: 116 sec



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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:10:55 ; Search time 13.3 Seconds

(without alignments)
1212.972 Million cell updates/sec

Title: US-09-826-509-449

Perfect score: 2292

Sequence: 1 MVPEPGPTANSTPAWGAGPP.....FNIDPAEPFLRPHPLGIFTN 440

Scoring table: Biosim62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs., 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	2287	99.8	440	1 S9H6_HUMAN	p50406 homo sapien
2	1989	86.8	440	1 S9H6_MOUSE	Q9Lc8 mus musculus
3	1678	73.2	436	1 S9H6_RAT	P31388 rattus norvegicus
4	591.5	25.8	466	1 B1AR_CANPA	P34971 canis familiaris
5	587.5	25.6	473	1 B1AR_RAT	P18090 rattus norvegicus
6	586.5	25.6	466	1 B1AR_FELCA	Q0T862 felis silvestris
7	571	24.9	474	1 B1AR_MACMO	P47899 macaca mulatta
8	563.5	24.6	480	1 B1AR_PIG	Q28998 sus scrofa
9	559	24.4	468	1 B1AR_CANPA	O02662 canis familiaris
10	555.5	24.4	405	1 B1AR_BOVIN	O9796 bos taurus
11	557.5	24.3	467	1 B1AR_HUMAN	P08588 homo sapiens
12	557	24.3	477	1 B3AR_BOVIN	P46626 bos taurus
13	554	24.2	405	1 B3AR_SHEEP	Q0XT58 ovis aries
14	553.5	24.1	400	1 B3AR_MOUSE	P25962 mus musculus
15	552.5	24.1	400	1 B3AR_HUMAN	P21728 homo sapiens
16	552.5	24.1	446	1 B3AR_SHEEP	Q8997 ovines aries
17	552.5	24.1	467	1 B3AR_RAT	P26255 rattus norvegicus
18	551.5	24.1	400	1 B3AR_CAPRI	Q0XT57 capra hircus
19	550.5	24.0	405	1 B3AR_MACMO	O77680 macaca mulatta
20	548.5	23.9	446	1 D1DR_CARAU	P35406 carassius auratus
21	547.5	23.9	363	1 D1DR_MACMO	Q28524 macaca mulatta
22	543.5	23.7	418	1 B3AR_FELCA	Q0T874 felis silvestris
23	539.5	23.5	398	1 DADR_PIG	P50130 sus scrofa
24	538.5	23.5	446	1 DADR_OREMO	P47800 oreochromis
25	538	23.5	386	1 B4AR_MELEGA	P43141 meleagris gallopavo
26	535.5	23.4	428	1 B4AR_MELEGA	P18901 rattus norvegicus
27	533.5	23.3	446	1 DADR_RAT	P13945 rattus norvegicus
28	531	23.3	408	1 B3AR_HUMAN	P42288 didelphis marsupialis
29	530.5	23.1	446	1 DADR_DIDMA	MIM: 601109; InterPro: IPR000276; GPCR_Rhodopsin
30	528.5	23.1	463	1 D5DR_FUGRU	DR P00001; 7tm_1; PRINTS; PRO1102; SHT6RCCEPTR.
31	526.5	23.0	483	1 B3AR_MELEGA	DR P07700 meleagris gallopavo
32	524.5	22.9	459	1 D1DR_FUGRU	DR Q53452 fugu rubripinnatus
33	524	22.9	351	1 B3AR_CAVPO	Q60483 cavia porcellus

ALIGNMENTS

RESULT 1

5H6_HUMAN STANDARD; PRT; 440 AA.

ID 5H6_HUMAN

AC P50406; Q11640;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE DE

GN 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR)

HTR6,

PROTEIN: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Homo sapiens (Human).

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Homo sapiens (Human).

OX NCBI_TaxId:9606;

RN [1]

RP SEQUENCE FROM N.A.

RN TISSUE=Striatum;

RX MEDLINE=95102917; PubMed=8522988;

RA Kohen R., MacCall M.A., Khan N., Druck T., Huebner K., Lachowicz J.E., Sibley D.R., Roth B.J., Hamblin M.W., "Cloning, characterization, and chromosomal localization of a human 5-HT6 serotonin receptor"; J. Neurochem. 66:47-56(1996).

RN [2]

RP SEQUENCE OF 215-280 FROM N.A.

RC TISSUE=Striatum;

RX MEDLINE=95102917; PubMed=8522988;

RA Ulmer C., Schmuck K., Kalkman H.O., Lubbert H.; RT "Expression of serotonin receptor mRNAs in blood vessels.";

RL FEBS Lett. 370: 215-221(1995).

CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOTGENIC HORMONE THAT FUNCTION AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MODERATED BY G PROTEINS THAT STIMULATES ADENYLATE CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN

CC -1- TISSUE SPECIFICITY: EXPRESSED IN SEVERAL HUMAN BRAIN REGIONS, MOST PROMINENTLY IN THE CAUDATE NUCLEUS.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC

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CC

CC EMBL; L41147; AAA92622; 1; -.

DR EMBL; 249119; CA88929; 1; -.

DR GCRDB; GCR_1062; -.

DR GCRDB; GCR_1885; -.

DR MIM: 601109; InterPro: IPR000276; GPCR_Rhodopsin.

DR P00001; 7tm_1; PRINTS; PRO1102; SHT6RCCEPTR.

P41596 drosophila

P02666 oryctolagus cuniculus

Q93127 balinus ampion

P97714 mus musculus

P2289 xenopus laevis

P25100 homo sapiens

P22290 xenopus laevis

Q24563 drosophila

Q42574 xenopus laevis

Q25188 heliothis vires

P21918 homo sapiens

DR	PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.	RN	[1] SEQUENCE FROM N.A.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.	RP	SEQUENCE FROM N.A.
FT	DOMAIN 1 34	RC	STRAIN=129/SVJ; TISSUE=Brain;
FT	TRANSMEM 35 57	RA	Kohen R., Guthrie C.R., Heidmann D.E.A., Hamblin M.W.;
FT	DOMAIN 58 64	RT	"Mutagenesis studies of the mouse 5-Ht6 serotonin receptor.";
FT	TRANSMEM 65 85	RL	Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
FT	DOMAIN 86 100	CC	-1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
FT	TRANSMEM 101 122	CC	HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION AS
FT	DOMAIN 123 144	CC	A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS
FT	TRANSMEM 145 166	CC	RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLYL CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS
FT	DOMAIN 167 184	CC	(BY SIMILARITY).
FT	TRANSMEM 185	CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
FT	DOMAIN 209 265	CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FT	TRANSMEM 266 290	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	DOMAIN 291 295	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
FT	TRANSMEM 296 320	CC	the European Bioinformatics Institute. There are no restrictions on its
FT	DOMAIN 321 440	CC	use by non-profit institutions as long as its content is in no way
FT	DISULFID 99 180	CC	modified and this statement is not removed. Usage by and for commercial
FT	CONFFLICT 247 247	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/) or send an email to licensee@isb-sib.ch).
SEQUENCE 440 AA; 46954 MW; C888F47650C1D2EF CRC64;			
Query Match 99.8%; Score 2287; DB 1; Length 440; Best Local Similarity 99.8%; Pred. No. 5.4e-17; Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 MVPEPGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60		DR	EMBL; AP134158; ADD46490.1; -.
Db 1 MVPEPGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60		DR	MG1; 1196627; Htr6.
QY 61 SNFFFLVSLFTSDLMLVGWVPPAMLNALYGRWLQLGCLWTFDVMCCSASILNLCL 120		DR	Pfam; PF00001; 7tm_1; 1.
Db 61 SNFFFLVSLFTSDLMLVGWVPPAMLNALYGRWLQLGCLWTFDVMCCSASILNLCL 120		DR	PROSITE; PS50237; G_PROTEIN_RECPT_F1_2; 1.
QY 121 SLDRLYLILSPRLRYKLRMPLRPLALVLGAWSLAALASFLPILLGHELGHARRPVPGQC 180		DR	PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
Db 121 SLDRLYLILSPRLRYKLRMPLRPLALVLGAWSLAALASFLPILLGHELGHARRPVPGQC 180		KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
FT DOMAIN 1 34		FT	TRANSMEM 35 57
FT DOMAIN 58 64		FT	TRANSMEM 65 85
FT DOMAIN 86 100		FT	TRANSMEM 101 122
FT DOMAIN 123 144		FT	TRANSMEM 145 166
FT DOMAIN 167 184		FT	TRANSMEM 185 208
FT DOMAIN 209 265		FT	TRANSMEM 293 297
FT DOMAIN 291 295		FT	TRANSMEM 322 327
FT DOMAIN 321 440		FT	DISULFID 99 180
FT CARBOHYD 9 9		FT	SEQUENCE 440 AA; 46954 MW; 4440CDEB0FEC CRC64;
QY 241 RTRPRPGEVADSRRLAKHRSRKALKASLTGILGMFVTLPEFVANIVAVCDICISP 300		QY	N-LINED (GLCNAC . . .) (POTENTIAL).
Db 241 RTRPRGVEVADSRRLAKHRSRKALKASLTGILGMFVTLPEFVANIVAVCDICISP 300		Db	1 MVPERGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
QY 301 LFDVLTWLGVCNSTMPITIPLMDFEKFRLGRFLPCPREREQASLASPLSLRHSGP 360		QY	1 MVPERGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
Db 301 LFDVLTWLGVCNSTMPITIPLMDFEKFRLGRFLPCPREREQASLASPLSLRHSGP 360		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
QY 361 RPGLSIQQVPLPLPPDSDSDAAGSGGSSGLRATQQLPGEATODPPLPTRAANVF 420		QY	1 MVPERGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
Db 361 RPGLSIQQVPLPLPPDSDSDAAGSGGSSGLRATQQLPGEATODPPLPTRAANVF 420		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
QY 421 FNIDPAPPEPLRPHPIGPTN 440		QY	1 MVPERGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
Db 421 FNIDPAPPEPLRPHPIGPTN 440		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
RESULT 2		QY	1 MVPERGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
5H6_MOUSE STANDARD; PRT; 440 AA.		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
AC Q9TC8; 20-AUG-2001 (Rel. 40, Created)		QY	1 MVPERGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
DT 20-AUG-2001 (Rel. 40, Last sequence update)		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
DT 20-AUG-2001 (Rel. 40, Last annotation update)		QY	1 MVPERGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
DE 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR).		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
GN HTR6.		QY	1 MVPERGPTANSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
OS Mus musculus (Mouse).		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		QY	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
NCBL_TaxID=10090;		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
OX		QY	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
QY 239 VPRHPRGVEVADSRRLAKHRSRKALKASLTGILGMFVTLPEFVANIVAVCDIS 298		Db	1 MVPERGPNVSTPAWGAGPPSAPGGSGWAAACWVIALTAANSLLIALCTQPALRNT 60
Query Match 86.8%; Score 1989; DB 1; Length 440; Best Local Similarity 87.6%; Pred. No. 2.7e-118; Matches 387; Conservative 15; Mismatches 36; Indels 4; Gaps 2;			

Db	431 DVGAAP-----PARLLEPWAGCNG----GAAAADSDSSIDEPGPGRP	466	FT MOD_RES 415 415 PHOSPHORYLATION.(BY CAPK) (POTENTIAL).
ID	B1AR_MACMU	STANDARD; PRT; 480 AA.	FT LIPID 395 395 PALMITATE (BY SIMILARITY).
AC	P47893;		FT SEQUENCE 480 AA; 51608 MW; 25C18FA03128084 CRC64;
RESULT	8		
ID			
AC			
DT	01-FEB-1995 (Rel. 33, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	BETA-1 ADRENERGIC RECEPTOR.		
GN	ADRB1.		
OS	Macaca mulatta (Rhesus macaque).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.		
OX	NCBI_TaxID=9544;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=95078456; PubMed=7987008;		
RA	Searles R.P., Nipper V.J., Machida C.A.;		
RT	"The rhesus macaque beta 1-adrenergic receptor gene: structure of the gene and comparison of the flanking sequences with the rat beta 1-adrenergic receptor gene.";		
RT	DNA Seq. 4:231-241(1994).		
CC	-!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATELY EQUAL AFFINITY.		
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-!- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDiated BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.		
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
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CC	-----		
DR	EMBL; X75540; CRA53228.1; -.		
DR	HSSP; P07700; IDEP.		
DR	GCRDB; GCR_1746; -.		
DR	InterPro; IPR00275; GPCR_Rhodopsin.		
DR	Prfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PRO0237; GPCR_RHODOPSIN.		
DR	PRINTS; PRO0103; ADRENERGIC.		
DR	PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.		
DR	PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.		
DR	G-protein coupled receptor; Transmembrane; Glycoprotein; KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.		
FT	DOMAIN 1 59 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 60 83 1 (POTENTIAL).		
FT	DOMAIN 84 96 2 (POTENTIAL).		
FT	TRANSMEM 97 120 2 (POTENTIAL).		
FT	DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 132 155 3 (POTENTIAL).		
FT	DOMAIN 156 175 4 (POTENTIAL).		
FT	TRANSMEM 176 199 EXTRACELLULAR (POTENTIAL).		
FT	DOMAIN 200 221 5 (POTENTIAL).		
FT	TRANSMEM 222 245 EXTRACELLULAR (POTENTIAL).		
FT	DOMAIN 246 328 CYTOSPLASMIC (POTENTIAL).		
FT	TRANSMEM 329 352 6 (POTENTIAL).		
FT	DOMAIN 353 359 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 360 383 7 (POTENTIAL).		
FT	DOMAIN 384 480 CYTOPLASMIC (POTENTIAL).		
FT	CARBHD 15 15 N-LINKED (GLCNAC . .) (PROBABLE).		
FT	DISULFID 131 209 BY SIMILARITY.		
FT	MOD_RES 315 PHOSPHORYLATION (BY CAPK) (POTENTIAL).		
RESULT	9		
ID	B1AR_PIG		
AC	028998; 046575;		
DR	15-JUL-1998 (Rel. 36, Created)		
DR	15-DEC-1998 (Rel. 37, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	BETA-1 ADRENERGIC RECEPTOR.		
GN	ADRB1.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=98318327; PubMed=9655595;		
RA	CAO H., Bidwell C.A., Williams S.K., Liang W., Mills S.E.; Williams J. Anim. Sci. 76:1720-1721(1998).		
RT	"Nucleotide sequence of the coding region for the porcine betal-adrenergic receptor gene.";		
RT	adrenergic receptor gene.";		
RL	J. Anim. Sci. 76:1720-1721(1998).		
RN	[2]		
RP	SEQUENCE OF 101-468 FROM N.A.		
RC	TISSUE=Heart;		
RC	McNeil R.L., Mersmann H.J.;		
RL	Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.		
CC	-!- FUNCTION: BETA ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATELY EQUAL AFFINITY (BY SIMILARITY).		
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-!- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDiated BY ITS		

CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
CC SIMILARITY).

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL; AE042454; ARB97525.1;
DR EMBL; U56425; AAC06330.1; -.
DR HSSP; P07700; IDEP.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; Yml_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR00561; ADRENGB3AR.
DR PRINTS; PRO103; ADRENERGICR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 83 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 84 96 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 97 121 2 (POTENTIAL).
FT DOMAIN 122 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 153 3 (POTENTIAL).
FT DOMAIN 154 176 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 177 197 4 (POTENTIAL).
FT DOMAIN 198 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 244 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 245 315 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 316 336 6 (POTENTIAL).
FT DOMAIN 337 347 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 348 368 7 (POTENTIAL).
FT DOMAIN 369 468 CYTOPLASMIC (POTENTIAL).
FT CARBOYD 15 475 N-LINKED (GLCNAC, . ,) (POTENTIAL).
FT DISULFID 131 208 BY SIMILARITY.
FT LIPID 382 382 PALMITATE (BY SIMILARITY).
FT CONFLICT 173 A -> AR (IN REF. 2).
FT CONFLICT 316 316 L -> V (IN REF. 2).
FT CONFLICT 326 326 CWL -> WWW (IN REF. 2).
FT CONFLICT 448 448 R -> A (IN REF. 2).
FT CONFLICT 458 458 T -> S (IN REF. 2).
FT CONFLICT 463 464 A -> SF (IN REF. 2).
FT SEQUENCE 468 AA; 50098 MW; 93CAEETBB70225 CRC64;

Query Match 24.4%; Score 559; DB 1; length 468;
Best Local Similarity 33.3%; Pred. No. 1.7e-28; Mismatches 149; Conservative 67; Indels 72; Gaps 15;

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CC or send an email to license@isb-sib.ch).

Db 262 RFLGLSPARRPPSPAPSPGSPILPAAAAAPVANGRTSKRRSPRLVALREQOKALK--TLGI 318
Db 273 LLGMFFVTVLPFWVANTVQAV-CDCTSPGLPFLVLTWGYCNSTMNPVLY--PLFMRDFK 328
Db 319 IMGVFTFLWLPFLANVVKAFHRDLYPDRLVFFNNLGIANSAFNPIYCRSP---DFR 374
QY 329 RALGRFPCCPQRQASLASPSLTSHSQSPRPGSLQQLVLPPLP---PDSDSDA 384
Db 375 KAFORLICCAR-----RVARGSCAACGDPGRASGCLAVARPPSPGAASHDDDEDV 427
QY 385 GSGGSSCLRLTQLLPP---GEATQD 407
Db 428 GAAP----PAPLBEWAGYNGGAARD 449

RESULT 10
B3AR_CANFA ID B3AR_CANFA STANDARD; PRT; 405 AA.
AC 002662; Q91P72;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE BETA-3 ADRENERGIC RECEPTOR.
GN ARDB3 OR B3AR.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxId=9615;
RN [1]
RN SEQUENCE FROM N.A.
RN MEDLINE=9909520; PubMed=9881593;
RA Thomson G.M., Kelly L.J., Candelier M.R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RA Archimbaud , Strosberg A.D.;
RT "Genomic cloning and species-specific properties of the recombinant
CC canine beta-3-adrenoceptor";
RT Eur. J. Pharmacol. 363:217-227(1999).
RN [2]
RN SEQUENCE FROM N.A.
RA Thomason G.M., Kelly L.J., Candelier M.R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE ACTION OF G-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G-
CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
CC THERMOGENESIS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC or send an email to license@isb-sib.ch).

DR EMBL; U92468; AAB51068.1; -.
DR EMBL; AF200597; AAB08307.1; -.
DR HSSP; P07700; IDEP.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR00563; ADRENGB3AR.
DR PROSITE; PRO103; ADRENERGICR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 37 63 1 (POTENTIAL).
FT DOMAIN 64 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT DOMAIN 92 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).

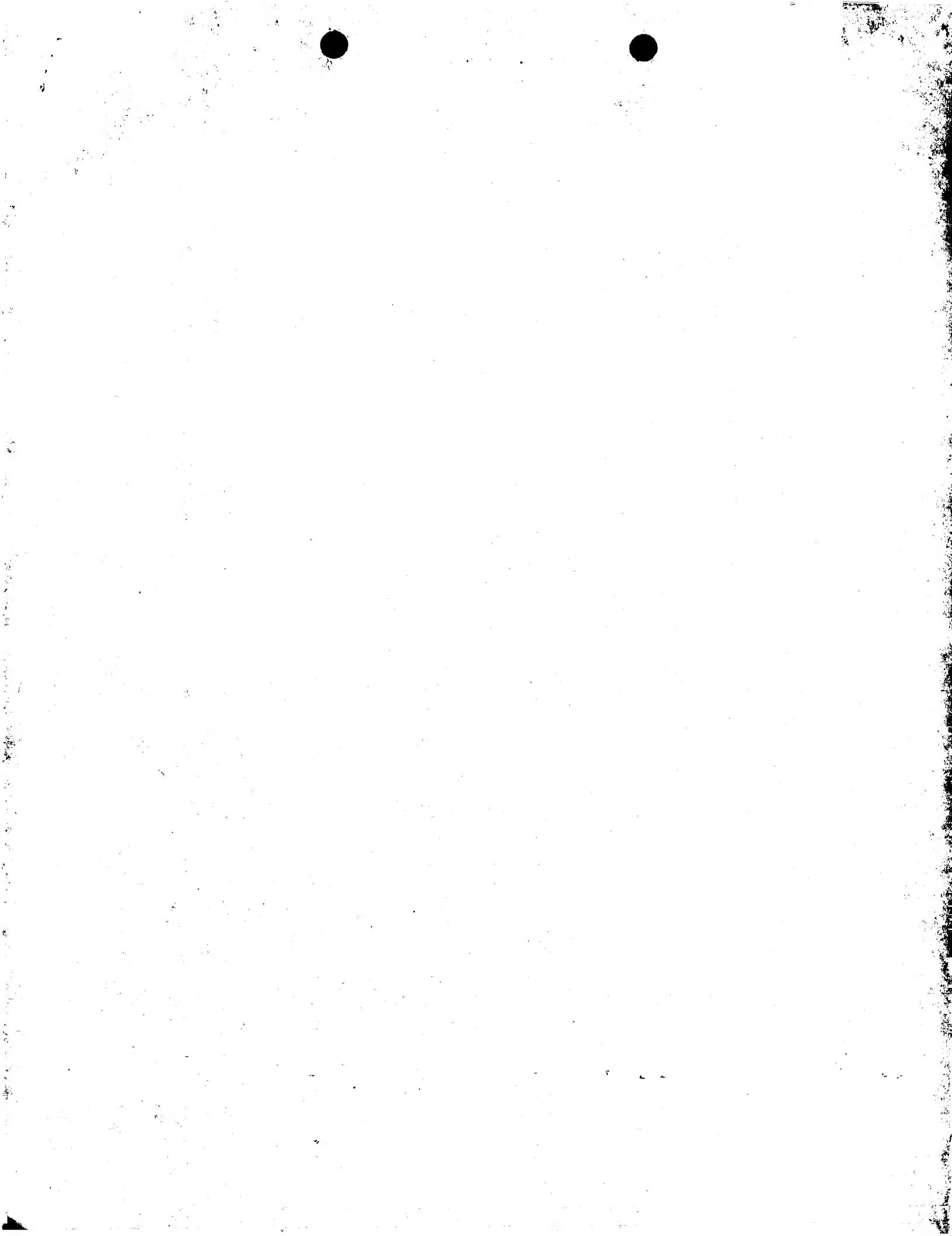
Db	150	CVIALDRYLATISPFYQOSULTRARARAVLCTWAIASLVSFLPIEMQWGDKDASRC	209
CC	---	SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	CC
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its	CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	210	VNDPECCOFINEGYAITSVSSVFSVPLCIMAFVLRVREAQKVKIDSCERRFLSGP	269
QY	230	ASQASETLQVPRTPRGVESADER-----RIATHKNSRKAALKLTGILGMFVVWL	282
QY	283	PFEVANTVQAV--CDCISPGLEDLTVIGYCNSTMNPITY--PLFMRFFKRALGRFLPCP	338
Db	326	PFPLANVVKAFFRDVLDPDFEVFNWLGYANSAFNPIYCRSP---DFRKAFORLICCA	381
Db	270	ARLPSPA-PSPGPPLPAATVANGRANKRPPRLVALREQKALK---TLGIMCVFTLWL	325
QY	339	REPREROASLASPLSLRSHGPRGLSQVQLPLPLPPSDSDSDAGGGSSLRLTAQL	398
Db	382	R-----RAACGSHAAAGDPRALGCLAVARRSPSGAASDDDDDDDDVGAAAPPVRL	434
QY	399	LIP-----GEATODPPLPTRAAG	417
CC	-	LIPWAGYNGGAANSDDSPDEPSRAGCA	462
RESULT	12		
ID	B1AR_HUMAN	STANDARD;	PRM; 477 AA.
AC	208588; Q9UKG8; Q9UKG7;		
DT	01-AUG-1988 (Rel. 08, Created)		
DT	20-AUG-2001 (Rel. 40, Last sequence update)		
DE	BETA-1 ADRENERGIC RECEPTOR.		
GN	ADRB1 OR ADRB1 OR B1AR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
RA	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
RA	[1]		
RN	NCBI_TaxId:9606;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Placenta;		
RX	MEDLINE-88068509; PubMed=2825170;		
RX	Frielle T., Collins S., Daniel K.W., Caron M.G., Lefkowitz R.J.,		
RA	Kobilka B.K.;		
RA	"Cloning of the cDNA for the human beta 1-adrenergic receptor."		
RA	Proc. Natl. Acad. Sci. U.S.A. 84:7920-7924(1987).		
RA	[2]		
RP	VARIANT ARG-39.		
RX	Medline=99230291; PubMed=10212248;		
RA	Mason D.A., More J.D., Green S.A., Liggett S.B.;		
RA	"A gain-of-function polymorphism in a G-protein coupling domain of the human beta1-adrenergic receptor";		
RA	J. Biol. Chem. 274:12670-12674(1999).		
RA	[3]		
RP	VARIANTS GLY-49 AND ARG-39.		
RX	Medline=99407239; PubMed=10477438;		
RA	Moore J.D., Mason D.A., Green S.A., Hsu J., Liggett S.B.;		
RT	"Racial differences in the frequencies of cardiac beta(1)-adrenergic receptor polymorphisms: analysis of c145A>G and c1165G>C.";		
RL	Hum. Mutat. 14:271-271(1999).		
RT	[4]		
RP	VARIANT GLY-49.		
RX	Medline=2050747; PubMed=11052857;		
RA	BorJesson M., Magnusson Y., Hjalmarsson A., Andersson B.;		
RT	"A novel polymorphism in the gene coding for the beta(1)-adrenergic receptor associated with survival in patients with heart failure.";		
RL	Eur. Heart J. 21:1833-1838(2000).		
RT	-- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYL CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATELY EQUAL AFFINITY.		
CC	-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.		
QY	1	MYPEPGPTANSTPAWGAGPPSAPGGSGWAALCVVIAVLAANSLILALICQPAIRNT	60
Db	33	LPAPSPAPSLPAPSEPEPLSQWTTAGMLILMALLIVAVGVNLVIVALAKTPRQLT	92
QY	61	SNFLVLSLFTSDLMVGLMPAAMLNLYGRVLAIGCLMATAFDWMCASILNLCL	120
Db	93	TNLFTMSLASADLVGLLWVPGATIIVWGRMEYGSFCELWTSVDLVCVTASIECVI	152
QY	121	SDRYLLTSLSPRYKRMPLRALVAGWASLAAASPLPLIGW--HELGHARPV--	176
Db	153	ALDRYLALITSPLVPLVSGLTFPLSGACIFCYCRLIAARKQAVQVAS---LTTGMAQ	212
QY	177	PGQCRLLASLPLVPLVSGLTFPLSGACIFCYCRLIAARKQAVQVAS---LTTGMAQ	232
Db	213	PRCCDFVNRAVAYAASSVSVFVPLCIMAFVLRVREAQKVKIDSCERRFLGQARP	272

Db	364 RPFHHLAAASPRAPS-----GAPMTMTSPKGPMQ-----PPEID----- 398
FT	LIPID 361 361 SEQUENCE 405 AA; 43032 MW; A2BAEAEABE98ADS CRC64;
SQ	Query Match 24.1%; Score 553.5; DB 1; Length 405; Best Local Similarity 34.3%; Pred. No. 3e-28; Matches 144; Conservative 56; Mismatches 165; Indels 55; Gaps 1
QY	B3AR_SHEEP STANDARD; PRT; 405 AA.
DB	09X758; ID 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
AC	DE BETA-3 ADRENERGIC RECEPTOR.
DT	ADRB3.
OS	Ovis aries (Sheep).
GN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
QC	NCBI_TaxID:9940;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MERINO;
RX	MEDLINE=20292453; PubMed=10834601;
RA	Forrest R.H.; Hickford J.G.H.;
RT	"Rapid communication: nucleotide sequences of the bovine, caprine, and ovine beta-3-adrenergic receptor genes.";
RL	J. Anim. Sci. 78:1397-1398(2000).
CC	-!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF C PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND THERMOGENESIS.
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR	EMBL: AF105928; AAC26147.1. -
DR	InterPro: IPR00276; GPCR_Rhodopsn.
DR	PRINTS: PR00563; ADRENRGCBAR.
DR	PROSITE: PS00237; G_PROTEIN_REC_EFL_1; 1.
DR	PROSITE: PS50262; G_PROTEIN_REC_EFL_2; 1.
KW	G-Protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT	DOMAIN 1 36 63 1 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 36 72 2 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 64 91 111 3 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 73 92 111 3 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 112 133 155 4 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 134 178 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 327 203 225 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 179 225 292 6 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 204 292 314 7 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	CARBONYD 348 405 8 5 (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 26 26 314 7 (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID 110 189 BY SIMILARITY.
RESULT 14	
QY	B3AR_SHEEP STANDARD; PRT; 405 AA.
DB	09X758; ID 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
AC	DE BETA-3 ADRENERGIC RECEPTOR.
DT	ADRB3.
OS	Ovis aries (Sheep).
GN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
QC	NCBI_TaxID:9940;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MERINO;
RX	MEDLINE=20292453; PubMed=10834601;
RA	Forrest R.H.; Hickford J.G.H.;
RT	"Rapid communication: nucleotide sequences of the bovine, caprine, and ovine beta-3-adrenergic receptor genes.";
RL	J. Anim. Sci. 78:1397-1398(2000).
CC	-!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF C PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND THERMOGENESIS.
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR	EMBL: AF105928; AAC26147.1. -
DR	InterPro: IPR00276; GPCR_Rhodopsn.
DR	PRINTS: PR00563; ADRENRGCBAR.
DR	PROSITE: PS00237; G_PROTEIN_REC_EFL_1; 1.
DR	PROSITE: PS50262; G_PROTEIN_REC_EFL_2; 1.
KW	G-Protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT	DOMAIN 1 36 63 1 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 36 72 2 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 64 91 111 3 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 73 92 111 3 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 112 133 155 4 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 134 178 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 327 203 225 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 179 225 292 6 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 204 292 314 7 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
FT	CARBONYD 348 405 8 5 (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 26 26 314 7 (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID 110 189 BY SIMILARITY.
RESULT 15	
QY	B3AR_MOUSE STANDARD; PRT; 400 AA.
DB	2276 MFTVTLPPFVNANIQAV--CDCISPGFLDVITWLGYCNSTNPMLY--PLFMDPKRA 330
AC	DE BETA-3 ADRENERGIC RECEPTOR.
DT	300 TETLCWLPFFVVNVNVRALGGPSLVSGLSGTFLANLWLGTRANSFAENPLYCRSP---DFRSA 355
OS	mus musculus (Mouse).
GN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SWISS;
RX	MEDLINE=92037534; PubMed=1718744;
RA	Nahmias C., Blin N., Elalouf J.M., Mattel M.-G., Strosberg A.-D., Emorine L.J.;
RT	"Molecular characterization of the mouse beta 3-adrenergic receptor: relationship with the atypical receptor of adipocytes.";
RL	EMBO J. 10:3721-3727(1991).
CC	[2]
DR	REVISIONS, SEQUENCE FROM N.A.
RX	MEDLINE=93279311; PubMed=8389293;
RA	van Spronsen A., Nahmias C., Krief S., Brriend-Sutren M.-M., Strosberg A.-D., Emorine L.J.;
RT	"The promoter and intron/exon structure of the human and mouse beta 3-adrenergic-receptor genes.";
RL	Eur. J. Biochem. 213:1117-1124(1993).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM B).
RC	STRAIN=C57BL/6; TISSUE=Brown adipose tissue;
RX	MEDLINE=93936494; PubMed=1045505;
RA	Evans B.A., Papaioannou M., Hamilton S., Summers R.J.;
RT	"Alternative splicing generates two isoforms of the beta3-adrenoceptor

RT which are differentially expressed in mouse tissues.";
 RL Br. J. Pharmacol. 127:1525-1531(1999).
 RN [4]
 RP SEQUENCE OF 378-400 FROM N.A.
 RC TISSUE:Adipose tissue;
 RX MEDLINE=93125503; PubMed=1336117;
 RA Granneman J.G., Lahmers K.N., Rao D.D.;
 RT Rodent and human beta 3-adrenergic receptor genes contain an intron
 within the protein-coding block";
 RL Mol. Pharmacol. 42: 964-970(1992).
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLYL CYCLASE THROUGH THE ACTION OF G PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
 CC THERMOGENESIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM A (SHOWN HERE) AND
 CC ISOFORM B; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES, AND DIGESTIVE TRACT. ISOFORM B HIGHEST IN BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR
 DR EMBL: X72862; CA051384; 1; -.
 DR EMBL: A0193027; AA05768; 1; -.
 DR EMBL: SS3290; AAB4836; 1; -.
 DR PIR: S18548; S18548.
 DR PIR: S32804; S32804.
 DR HSSP: P07700; IDEP; -.
 DR GCRdb; GCR_0253; -.
 DR GCRdb; GCR_0551; -.
 DR GCRdb; GCR_0708; -.
 DR MGD: MG1:87939; Adrb3.
 DR InterPro: IPR000216; GCR_Rhodopsn.
 DR Pfam: PF00001; 7tm; 1.
 DR PRINTS: PR00237; GPCRKHODPSN.
 DR PRINTS: PR01103; ADRENICGB3AR.
 DR PROSITE: PS00237; G_PROTEIN_REC_EF1_2; 1.
 DR PROSITE: PS0262; G_PROTEIN_REC_EF1_2; 1.
 KW G-Protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate;
 KW Alternative splicing.
 FT DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 37 60 1 (POTENTIAL).
 FT DOMAIN 61 69 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 70 88 2 (POTENTIAL).
 FT DOMAIN 89 108 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 109 130 3 (POTENTIAL).
 FT DOMAIN 131 152 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 153 175 4 (POTENTIAL).
 FT DOMAIN 176 200 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 201 222 5 (POTENTIAL).
 FT DOMAIN 223 289 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 290 311 6 (POTENTIAL).
 FT DOMAIN 312 323 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 324 344 7 (POTENTIAL).
 FT DOMAIN 345 400 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFO 26 186 BY SIMILARITY.
 FT LIPID 107 358 PALMITATE (BY SIMILARITY).
 FT VARSPLIC 388 400 RFQGYEGARPFPT -> SSLRPRHLYTCLGVP (IN ISOFORM B);
 SQ SEQUENCE 400 AM: 43006 MW: 374E072C01DA32E CRC64;

Query Match	24 1%	Score 552.5;	DB 1;	Length 400;
Best Local Similarity	35 1%	Pred No. 3.8e-28;		
Matches	141;	Conservative	60;	Mismatches 150;
		Indels	51;	Gaps 15;
OY	5	PGPANSTPPA-WGAGP--PSAPGGSG----RWAALCYWIAL-TAANSLLIAJCTQ	54	
Db	3	PWPWRNGSLALWSADAPTLPDSAAANTSGLGVPAALAGALLALATVGNNLVLITART	62	
OY	55	PALRNTSNFLVLSIFTSIDLINVGLVMPPPMLNAYGRWLRGICLIMWAFDWMCCSASI	114	
Db	63	PRIQQTINFEVTSLAADLWGLVMPGCATLGHRRPLGEGLCEWISVWLCVTAASI	122	
OY	115	LNICLISLQRYLILTSPLRYKLRTPLRALKLVGASLALASFLPLLGWHLG---	170	
Db	123	ETLCALAVDRYLAUTNPLRKGTLVTRRAAVLVWIVSAAVSFAPIMSWWRVGADAE	182	
OY	171	---	226	
Db	183	AQEHSNPRC--CSFASNMPYALLSSSVFYLPLVMFLFVYARVFVAKROR-HLLRE	238	
OY	227	TGMASQASETQLQPRTPRP-----GVESADSR--RLATKHSKAALKATLGILL	274	
Db	239	LGRSPESPPSPSSRSPBGTGPAAPGVPGPCGRPARBLPRLREHAL--TUGLM	295	
OY	275	GMFFVTWLFPEVANIQAVC--DCISPLGFDVJWLGYCNSTMANPIY--PLFMRDR	329	
Db	296	GIFSLCWLFPEFLANVLRLAGLPSLVPSVFIALNWLGTAFAFNPNVYCRSPDFRDAFR	355	
OY	330	AL---GRPLPCPRC--PRERASLASPSLR--TSHGPPR	362	
Db	356	LICSYGGROPEEPRAVTFASPVEARQSPPLNRFDGEGARP	397	

Search completed: March 15, 2002, 14:14:26
 Job time: 211 sec



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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:08:55 ; Search time 17.53 Seconds
(without alignments)
1911.968 Million cell updates/sec

Title: US-09-826-509-449
Perfect score: 2292
Sequence: 1 MVPEPGPTANSTPAWGAGPP FNIDAPAEPELRPHPLGIPTN 440
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : PIR 68;*
1: pirl1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description	RESULT	1
1	2287	99.8	440	2 JC5520	serotonin receptor 6 - human	JC5520	
2	1899.5	82.9	437	2 I57942	5-hydroxytryptamine serotonin receptor	N;Alternate names: 5-hydroxytryptamine receptor 6 (5-HTR6)	
3	1679.8	73.2	436	2 JN0591	serotonin receptor	C;Species: Homo sapiens (man)	
4	591.5	25.8	466	2 S36794	beta-1-adrenergic	C;date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999	
5	581	25.3	464	2 S12591	beta-1-adrenergic	C;Accession: JC5520	
6	563.5	24.6	480	2 I53053	beta-1-adrenergic	R;Kohen, R.; Metcalf, M.A.; Khan, N.; Druck, T.; Huebner, K.; Lachowicz, J.B.; Meltze	
7	557	24.3	477	1 QRHUB1	beta-1-adrenergic	J. Neurochem. 66: 47-56, 1996	
8	554	24.2	405	2 S52459	beta-3-adrenergic	A;Title: Cloning, characterization, and chromosomal localization of a human 5-HT 6 se	
9	552.5	24.1	400	2 S32804	beta-3-adrenergic	A;Reference number: JC5520; MUID:96102917	
10	552.5	24.1	446	1 DRYUD1	dopamine receptor	A;Molecule type: mRNA	
11	551.5	24.1	400	2 A41679	dopamine receptor	A;Cross-references: GB:L41147; NID:q1162923; PIDN:AAA92622.1; PID:q1162924	
12	551.5	24.1	400	2 A53281	dopamine receptor	A;Experimental source: brain	
13	547.5	23.9	363	2 I50475	dopamine D1 receptor	C;Comment: This protein shows high affinity for several therapeutically important ant	
14	543.5	23.7	418	2 G02953	beta-3-adrenergic	C;Genetics:	
15	538.5	23.5	446	2 I47217	dopamine receptor	A;Gene: HTR6	
16	538	23.5	386	2 S72168	dopamine receptor	A;Map position: 1p35-36	
17	535.5	23.4	428	2 A55044	beta-3-adrenergic	A;Introns: 238/3; 291/3	
18	533.5	23.3	487	1 DFRD1	dopamine receptor	C;Superfamily: vertebrate rhodopsin	
19	531	23.2	408	1 ORIUBE	beta-3-adrenergic	C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran	
20	531	23.2	414	1 ORIUB3	dopamine receptor	F:28-51;Domain: transmembrane #status predicted <TM2>	
21	528.5	23.1	463	2 B58849	dopamine receptor	F:100-123;/domain: transmembrane #status predicted <TM3>	
22	526.5	23.0	483	2 A25896	dopamine receptor	F:143-166;/domain: transmembrane #status predicted <TM4>	
23	525	22.9	385	2 S65780	dopamine receptor	F:185-208;/domain: transmembrane #status predicted <TM5>	
24	524.5	22.9	459	2 A58849	dopamine receptor	F:266-289;/domain: transmembrane #status predicted <TM6>	
25	521.5	22.5	511	2 S44275	dopamine receptor	F:298-321;/domain: transmembrane #status predicted <TM7>	
26	508	22.2	379	2 J66178	serotonin receptor	F:10/Binding site: carbohydrate (Asn) (covalent) #status predicted	
27	507.5	22.1	560	2 A8731	alpha-1A adrenergic	Query Match 99.8%; Score 2287; DB 2; Length 440;	
28	504	22.0	451	1 M15659	dopamine receptor	Best Local Similarity 99.8%; Pred. No. 8.6e-17; Matches 439; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
29	503	21.9	572	1 I39369	dopamine receptor	Db 1 MYPEPGPTANSTPAWGAGPPSAPGGPSAGGSGWAAALCVVIALTAANSLLJALICTOPALRN 60	

RESULT 3

JN0591 RTPRGVESADSRRLATKHSRKALKLTLGILGMFVWLPFFVANTIVQAVCDCISPG 300 serotonin receptor 6 - rat

N;Alternate names: 5-hydroxytryptamine receptor 6 (5-HT₆)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999

C;Accession: JN0591

R;Ruat, M.; Traiffort, E.; Arrang, J.M.; Tardivel-Lacome, J.; Diaz, J.; Leurs, R.; Bichem, Biophys. Res. Commun. 193, 268-276, 1993

A;Title: A novel rat serotonin (5-HT₆) receptor: molecular cloning, localization and A;Reference number: JN0591; MUID:93277562

A;Accession: JN0591

A;Molecule type: DNA

A;Cross-references: 1-36 <RUA>

A;Residues: 1-36

A;Cross-references: GB:562043; NID:9316608

A;Genetics:

A;Introns: 238/3

C;Superfamily: Vertebrate rhodopsin

C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein

F;29-53/Domain: transmembrane #status predicted <TM1>

F;63-84/Domain: transmembrane #status predicted <TM2>

F;95-112/Domain: transmembrane #status predicted <TM3>

F;141-168/Domain: transmembrane #status predicted <TM4>

F;185-213/Domain: transmembrane #status predicted <TM5>

F;267-293/Domain: transmembrane #status predicted <TM6>

F;297-319/Domain: transmembrane #status predicted <TM7>

F;9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.2%; Score 1678; DB 2; Length 436;

Best Local Similarity 91.7%; Pred. No. 1.3e-122;

Matches 322; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

Query Match 82.9%; Score 1899.5; DB 2; Length 437;

Best Local Similarity 84.5%; Pred. No. 9e-140;

Matches 376; Conservative 11; Mismatches 45; Indels 13; Gaps 4;

Query 1 MVPERGPTANSTPANGAGPPSAPGGSGWVAALCVVITALTAANSLLTALICTOPALRNT 60

Db 1 MVPEPGOPTANSTPANGAGPPSAPGGSGWVAALCVVITALTAANSLLTALICTOPALRNT 60

Query 61 SNEFLYSLFSDLMGLVWPPAMINALGRWLARGLCIWTADVMCCSASTLNCLLI 120

Db 61 SNEFLYSLFSDLMGLVWPPAMINALGRWLARGLCIWTADVMCCSASTLNCLLI 120

Query 61 SNEFLYSLFSDLMGLVWPPAMINALGRWLARGLCIWTADVMCCSASTLNCLLI 120

Db 61 SNEFLYSLFSDLMGLVWPPAMINALGRWLARGLCIWTADVMCCSASTLNCLLI 120

Query 121 SLDRYLILSLPLRYKURMTPRLAVALVLGWSLAAASLEPLLIGLWHELGHARPPVGOC 180

Db 121 SLDRYLILSLPLRYKURMTPRLAVALVLGWSLAAASLEPLLIGLWHELGHKARTPVGOC 180

Query 181 RLLASLPFLVAVSGTFFLPSGAICFTYCILLAAARKQAVQAVASLTGTGMAQSASETLOQP 240

Db 181 RLLASLPFLVAVSGTFFLPSGAICFTYCILLAAARKQAVQAVASLTGTGMAQSASETLOQP 240

Query 241 RTPRGVESADSRRLATKHSRKALKLTLGILGMFVWLPFFVANTIVQAVCDCISPG 300

Db 241 RTPRGVESADSRRLATKHSRKALKLTLGILGMFVWLPFFVANTIVQAVCDCISPG 300

Query 301 LFDVLTWLGNCNSTMPNIPYPLFMRDFKRALGRFLPCPRPRERASLSPL---RT 355

Db 301 LFDVLTWLGNCNSTMPNIPYPLFMRDFKRALGRFLPCPRPRERASLSPL---RT 355

Query 356 SHSGRRPGLSLQQVPLPLPPDSDSDAQGGGGSLRLTAQLLIPGEATQDPLPPIPTRAA 415

Db 357 ORCQTRP-OLQQLQVPLPLPPDSDSDAQGGTSGLQLTAQLLIPGEATQDPLPPIPTRAA 415

Query 416 AAVNFTIDAEPEPLRPHPIGPTN 440

Db 413 TVVNFVFVTDSEPELRPHPIGPTN 437

RESULT 4

S36794 RTPRGMESADSRRLATKHSRKALKLTLGILGMFVWLPFFVANTIVQAVCDCISPG 300

C;Species: Mus musculus (house mouse)

C;Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999

C;Accession: S36794

R;Jasper, J.R.; Link, R.E.; Chruscinski, A.J.; Kobilka, B.K.; Bernstein, D. Biochim. Biophys. Acta 1178, 307-309, 1993

A;Title: Primary structure of the mouse beta(1)-adrenergic receptor gene.

A;Reference number: S36794; MUID:93372116

A;Accession: S36794

A;Status: Preliminary

A;Molecule type: DNA

QY 176 V-PGQCRLLIASLSPVPLVAGLFFELPSGAICFTYCRILAAKRCQAVQAS---LTIGM 229
Db 210 YNDPKCQDFVNRAVIAASSWVSVFVPLCIMAFVYLVRFREAQKVKKIDSCERFLGGP 269
QY 230 ASQAE-----LQVPTPRPGVESAD-----RRLATKHSKALKAK 267
Db 270 ARPPSPSPSPSPSPSPSPVAPPPGPPRPAAAATAPLVLNGRAGKRRPSRVALREKALK-- 327
QY 268 LTLGILGLGMFVTVNLPFFVANIVAV-CDCISPGSLFDVLTWLGVCNSTMNPITY--PLF 323
Db 328 -TIGLIMGVFTLCKLPUFLFLNVAARRHAAHGDPRASGCLARP-----PPSPGAASDDDDDVGA 435
QY 324 MRDKRKLGRFLPPRCPREROASLASPLSLRTSISGPRGLSIQQLVLPPLP-PDSDS 382
Db 385 --DFRNAFORLCCARRAARRHAAHGDPRASGCLARP-----PPSPGAASDDDDDVGA 435
QY 383 DAGGGSSGLRL 394
Db 436 DDVVGATOPRL 447

RESULT 7

ORHBL1
beta-1-adrenergic receptor - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 22-Jun-1999
C;Accession: A39911
R;Frielle, T.; Collins, S.; Daniel, K.W.; Caron, M.G.; Lefkowitz, R.J.; Kobilka, B.K.
Proc. Natl. Acad. Sci. U.S.A. 84, 7920-7924, 1987
A;Title: Cloning of the cDNA for the human beta-1-adrenergic receptor.
A;Reference number: A39911; MUID: 8868509
A;Accession: A39911
A;Molecule type: mRNA
A;Residues: 1-477 <PRT>
A;Cross-references: GB:J30319; NIDB:g178199; PIDN:AAA51667.1; PIB:g178200
C;Genetics:
A;Gene: GDB:ADRB1; ADRB1
A;Cross-references: GDB:119654; OMIM:109630
A;Map position: 10q25-10q25
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;59-84/domain: transmembrane #status predicted <TM1>
F;94-121/domain: transmembrane #status predicted <TM2>
F;133-154/domain: transmembrane #status predicted <TM3>
F;177-199/domain: transmembrane #status predicted <TM4>
F;224-245/domain: transmembrane #status predicted <TM5>
F;325-345/domain: transmembrane #status predicted <TM6>
F;358-377/domain: transmembrane #status predicted <TM7>
15/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.3%; Score 557; DB 1; Length 477;
Best Local Similarity 33.8%; Pred. No. 1e-35;
Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;

QY 1 MVPPPGPTANSTPAWGAGGPPSAPGGSGWVAALCGVIALTAANNSLLALICTOPALRN 60
Db 33 LVPRSSPASLPLPPASESPEPLSQONTAGWGLLMLALIVLIVAGNLVTAIAKTPRLQT 92
QY 61 SNPFVLSLTSPLDMGLVWMPAMLNALYGRWVIALRGCLLWFADWMCSCASILNLCI 120
Db 93 TNLFRTMSLASADVLNGLVLVPGFTAVVWGRWEVGFSCELMVSDVLCVTASITLCV 152
QY 121 SLDRYLLISPLRKLRLPMLRALVLGAWSLAASPLFLIGW- HELGHRRPV- 176
Db 153 ALDPYLAITSFPRQLSULTRARARGLVWVATASALVSLEPLIMHWWRASDEBRCYND 212
QY 177 PGOCRLLASLPLPVFVAVASGLTFFLPSGATCTFYCHILLAARKQAVQAS---LTGMA 232
Db 213 PKCCDFEVINRAYIAASSVVSFVYELCIMAFVYLVRFREAQKVKKIDSCERRFLGGP 272
QY 233 ASE-----LQPRTPPGVSAAS-----RRLATKHSKALKAKLGT 273

RESULT 8

S65459
beta-3-adrenergic receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Oct-1995 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999
C;Accession: S65459; S40504; S31659
R;Pietri-Rouxel, F.; Lenzen, G.; Kapoor, A.; Drumare, M.F.; Archimbaud, P.; Strosberg, J.; Biochem. 230, 350-358 1995
A;Title: Molecular cloning and pharmacological characterization of the bovine beta3-a
A;Reference number: S65459; MUID: 95324546
A;Accession: S65459; MUID: 95324546
A;Molecule type: mRNA
A;Residues: 1-405 <PTE>
A;Cross-references: EMBL:X85961; NID:9757758; PIDN:CAA59937.1; PIB:9757759
A;Experimental source: brown adipose tissue
R;Castellina, L.; Muzzin, P.; Revelli, J.P.; Ricquier, D.; Giacobino, J.P.
Biochem. J. 297, 93-97, 1994
A;Title: Expression of beta(1)- and beta(3)-adrenergic-receptor messages and adenylyl
A;Residues: 1-405 <PTE>
A;Reference number: S40503; MUID: 94107292
A;Accession: S40504
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Residues: 162-298 <CAS>
R;Stoffel, B.; Meyer, H.H.D.
submitted to the EMBL Data Library, June 1992
A;Description: Bovine beta3-adrenergic receptor, partial genomic sequence.
A;Reference number: S31659
A;Accession: S31659
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 4-5, 'HE', 8-105 <SMO>
A;Cross-references: EMBL:X67714
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; trans
F;37-63/domain: transmembrane #status predicted <TM1>
F;73-101/domain: transmembrane #status predicted <TM2>
F;113-133/domain: transmembrane #status predicted <TM3>
F;156-179/domain: transmembrane #status predicted <TM4>
F;204-225/domain: transmembrane #status predicted <TM5>
F;293-314/domain: transmembrane #status predicted <TM6>
F;327-347/domain: transmembrane #status predicted <TM7>
F;8,26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.2%; Score 554; DB 2; Length 405;
Best Local Similarity 33.6%; Pred. No. 1.5e-35;
Matches 143; Conservative 61; Mismatches 156; Indels 66; Gaps 13;

QY 1 MVPPPG-PRPANSTPAWGAGGPPSAPGGSGWVAALCGVIALTAANNSLLALICTOPALRN 59
Db 11 LTPWPDIPDPLAPNTANASGLPVGWVAVALAGALLALAVLATVGGGLNLVVAIAKTPRLQT 70
QY 60 TSNFVLSLTSPLDMGLVWMPAMLNALYGRWVIALRGCLLWFADWMCSCASILNLCI 119
Db 71 MTNVFTSLATDLVGLVWPGATLALGHWPLGVTCCLWMSVDVLCVTASIELCA 130
QY 120 ISDRYLLISPLRKLRLPMLRALVLGAWSLAALASFPLLLGWHLG-----H 171

RESULT 9

Db 131 LAVRYLAVTNPLRIGALVTRRLAALAVLVWVVAASVAFAPIMKWNRIGADEAORC 190

Db 172 ARPPVGQCRLLASLIPFVIVASGLTFFLPSGATCTYCRILLAARKAQAVVASITGM.. 229

Db 191 SNPPRC--CTFAANMPYLASSSFSYIPLVLMFVYARVVFVATRQLRLRERGRP 246

QY 230 -----ASQASETLQVPRTPRGVESADSR--RLATKHSRKAKAKLTGLIGMRFV 279

Db 247 PERSPPASRSRGSGLAGPCASPAGPGVSPYGRPARLPLREHRAU--TLGLIMTT 303

QY 280 TWIFFFVANIWOAV--COCISPGFLDVLTWLGICNSTMPLIY--PLFMRDRKRAJGF 334

Db 304 CWLFVFVNVNVRALGGPSLVSQPTFLNLWLGYANSAFNPLIXCRSPDERSAFLRLCRC 363

QY 335 LP-----CPRPRERQASLASPLSLRSHSRRPGLSLLSQWLPLPQDSSSDAGS 386

Db 364 RPEBHLAASAPPRLPS----GAPTAITSPAGPM-----PPELD----- 398

QY 387 GGSSGL 392

Db 399 GASCGL 404

RESULT 9

S32804

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 13-Aug-1999

C;Accession: S32804; S32827; S18348

R;Emorine, L.J.

R;submitted to the EMBL Data Library, March 1993

A;Reference number: S32803

A;Accession: S32804

A;Molecule type: DNA

A;Residues: 1-400 <EMO>

A;Cross-references: EMBL:X77862; PIDN:CAA51394.1; PID:9298113

R;van Spronsen, A.; Nahmias, C.; Krief, S.; Briend-Sutren, M.M.; Strosberg, A.D.; Emorine, J. Blochem, 213, 1117-1124, 1993

A;Title: The promoter and intron/exon structure of the human and mouse beta-3-adrenergic receptor: relationships

A;Reference number: S32826; MUID:92037311

A;Accession: S32827

A;Molecule type: DNA

A;Residues: 1-8;341-347;380-400 <SSPR>

R;Nahmias, C.; Blin, N.; Elalouf, J.M.; Mattei, M.G.; Strosberg, A.D.; Emorine, L.J. EMBO J. 10, 3721-3727, 1991

A;Title: Molecular characterization of the mouse beta-3-adrenergic receptor: relationships

A;Reference number: S10548; MUID:92037534

A;Accession: S10548

Molecule type: DNA

Residues: 1-388 <NAH>

A;Cross-references: EMBL:X60438; NID:950109; PIDN:CAA42966.1; PID:950110

C;Genetics:

A;Map position: 8A2-4

A;Introns: 38B/2

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

QY 5 PGPPANSIPA-WGGP--PSAPPGSG----WWAALCWVIAL-TAMANSLILALICTQ 54

RESULT 10

DYHUDI

dopamine receptor D1 - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C;Accession: S11377; S11376; S11379

R;Zhou, Q.Y.; Grandy, D.K.; Thambi, L.; Kushner, J.A.; van Tol, H.H.M.; Cone, R.; Pri Nature 337, 76-80, 1990

A;Title: Cloning and expression of human and rat D(1) dopamine receptors.

A;Reference number: S11377; MUID:90370094

A;Accession: S11377

A;Molecule type: DNA

A;Residues: 1-446 <ZHO>

A;Cross-references: EMBL:X58987

R;Dearby, A.; Gingrich, J.A.; Falardeau, P.; Freneau Jr., R.; Bates, M.D.; Caron, M Nature 347, 72-76, 1990

A;Title: Molecular cloning and expression of the gene for a human D(1) dopamine receptor

A;Reference number: S11376; MUID:90370093

A;Accession: S11376

A;Molecule type: DNA, mRNA

A;Residues: 1-446 <DEA>

A;Cross-references: EMBL:X55760; NID:930396; PIDN:CAA39286.1; PID:930397

R;Sunahara, R.K.; Niznik, H.B.; Weiner, D.M.; Stormann, T.M.; Brann, M.R.; Kennedy, J Nature 341, 80-83, 1990

A;Title: Human dopamine D(1) receptor encoded by an intronless gene on chromosome 5.

A;Reference number: S11379; MUID:90370095

A;Accession: S11379

A;Molecule type: DNA

A;Residues: 1-446 <SUN>

A;Cross-references: GB:X55758; NID:9288931; PIDN:CAA39284.1; PID:9288932

C;Genetics:

A;Gene: GDB:DR01

A;Cross-references: GDB:125240; OMIM:126449

A;Map position: 5q4-5q5

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter receptor

F;61-87/Domain: transmembrane #status predicted <TM1>

F;28-49/Domain: transmembrane #status predicted <TM2>

F;98-119/Domain: transmembrane #status predicted <TM3>

F;1-10-130/Domain: transmembrane #status predicted <TM4>

F;133-176/Domain: transmembrane #status predicted <TM5>

F;201-222/Domain: transmembrane #status predicted <TM6>

F;324-344/Domain: transmembrane #status predicted <TM7>

F;8;26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.1%; Score 552.5; DB 2; Length 400;

Best Local Similarity 35.1%; Pred. No. 1.9e-35;

Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

QY 5 PGPPANSIPA-WGGP--PSAPPGSG----WWAALCWVIAL-TAMANSLILALICTQ 54

F;194-214/Domain: transmembrane #status predicted <TM5>

F;215-273/Domain: intracellular #status predicted <CYT>

F;274-295/Domain: transmembrane #status predicted <TM6>

F;313-333/Domain: transmembrane #status predicted <TM7>

F;5175/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;96-186/Disulfide bonds: #status predicted

Db 239 LGRRPPEESPRSPRSRSPSPATVGTPTASDGIVSQRPARLPLGEHRLR--TLGLIM 295
 Qy 275 GMFVTFWLPFFVNVNIQAVC--DCISGFLFDVITLWLGYCNSTMPIY--PLFMRDFKR 329
 I: || : || || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 296 GITSLCWLPLPEFLANVLRAVLGVPSLVPSCVFIANWLGYANSANPFLYCRSPDFRDFAFR 355

Qy 330 AL---GRFLPCPRC--PRERQASLASPLR-TSHSGPRP 362
 I: || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 356 LIGSYGCRGPEEVVTPASPVASQNSPLNRFDGYEGERP 397

RESULT 13

150475

dopamine D1 receptor - goldfish

C;Species: Carassius auratus (goldfish)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999

C;Accession: I50475

R;Email: D.E.; Manelli, A.M.; Witte, D.G.; Lin, C.W.; Staffey, M.E.; Mackenzie, R.G.

M.J.; Pharmacol. 44, 1113-1118, 1993

A;Title: Cloning and characterization of a truncated dopamine D1 receptor from goldfish

A;Reference number: I50475; MUID:94088471

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-363 <FRA>

A;Cross-references: GB:L08602; NID:g212949; PIDN:AAA16322.1; PID:g212950

C;Keywords: neurotransmitter receptor

Query Match 23.7%; Score 543.5; DB 2; Length 418;
 Best Local Similarity 34.0%; Pred. No. 9.8e-35; Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

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Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Matches 144; Conservative 63; Mismatches 154;

Indels 63; Gaps 15;

Query Match 23.9%; Score 547.5; DB 2; Length 363;
 Best Local Similarity 37.1%; Pred. No. 4.1e-35; Indels 11; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Query Match 23.9%; Score 547.5; DB 2; Length 363;
 Best Local Similarity 37.1%; Pred. No. 4.1e-35; Indels 11; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Query Match 23.9%; Score 547.5; DB 2; Length 363;
 Best Local Similarity 37.1%; Pred. No. 4.1e-35; Indels 11; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Query Match 23.9%; Score 547.5; DB 2; Length 363;
 Best Local Similarity 37.1%; Pred. No. 4.1e-35; Indels 11; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Query Match 23.9%; Score 547.5; DB 2; Length 363;
 Best Local Similarity 37.1%; Pred. No. 4.1e-35; Indels 11; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Matches 127; Conservative 63; Mismatches 119;

Indels 33; Gaps 11;

Query Match 23.9%; Score 547.5; DB 2; Length 446;
 Best Local Similarity 30.9%; Pred. No. 2.6e-34; Indels 67; Gaps 14;
 Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Query Match 23.9%; Score 547.5; DB 2; Length 446;
 Best Local Similarity 30.9%; Pred. No. 2.6e-34; Indels 67; Gaps 14;
 Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Query Match 23.9%; Score 547.5; DB 2; Length 446;
 Best Local Similarity 30.9%; Pred. No. 2.6e-34; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

Matches 142; Conservative 78; Mismatches 173; Indels 67; Gaps 14;

C;Genetics:

A;Intron: 402/1

C;Superfamily: vertebrate rhodopsin

C;Genetics:

A;Intron: 402/1

C;Superfamily: vertebrate rhodopsin

QY	129	LSPRYKLMRPTPLRALALVGLGANSALAFLPLLGPHELHARPPVG-----	178
Db	126	SSPFERYEKKMTPKAFTLISVANTLWVJISFIPVQLSMHK--AKPTPSDGNVTSLGK	1822
QY	179	-OCLRILASLPFWLVASGIFTFLPSGATCTFYCRILLARKQWQVQASL-TTOMASQASE	2355
Db	183	THNCDSSLRSTYRAISSSIISFYIPVAIMIVTYRIYRAQORTIRISALERAAVHAKNCQ	2422
QY	236	TLCQVPRTPRGVSAADSNDRATHSKRKAUKAKLTGTLGFLGFMVTFWLFVVANIOVAD	2955
Db	243	TFLAGNGNPACSOPESSERKMSFKRETKLK--TLSVGMGVFCWCWFILCMVPGC	2999
QY	296	-----CISPGFLFDVLTLWLGICNSTMNPILYPLFLMRDFKRALGRFLPCPR-CPREROAS	3471
Db	300	SGETKPFCDISTFDFVFWFGWANSNLNPITY-AFNADFRKAFTSTLGCYRCIPLCPTSTNA-	3577
Qy	348	LASPRL-----TSHGSPRPLSLOQVPLPLPDDSDAGGGSSGLRLTAQLL 4000	
b	358	IETVSIINNGAVFWFSSKHFRRGFSKDCNLVYLIPHAVGSSSELDKKEBAGGIASPLEKL	417
QY	401	PGEATQDPPLPTRAABAVNFNIDPAEPLRP-----HP 434	
418	P-----	ALSVIJDYDVSLEKIQPITQONQHP 445	
Db			

Search completed: March 15, 2002, 14:10:49
Job time: 114 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Om protein - protein search, using sw model

Run on: March 15, 2002, 14:10:35 ; Search time 25.52 Seconds
(without alignments)
2521.937 Million cell updates/sec

Title: US-09-826-509-449

perfect score: 2292

Sequence: 1 MVPEPGPTANSTPAWGAGPP.....FNIDPAEPELRPHPLGIFTN 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_17:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2025	88.4	438	11 Q63004 ratus norv
2	578	25.2	405	11 Q9CRR2 mus musculu
3	563.5	24.6	405	6 Q9GL56 ovis arries
4	559.5	24.4	405	6 Q9GJS6 ovis arries
5	558.5	24.4	405	6 Q9GJ0 ovis arries
6	556	24.3	405	6 Q9GL57 ovis arries
7	546.5	23.8	402	5 Q4A198 apis mellif
8	540.5	23.6	407	6 Q9M200 sus scrofa
9	535	23.3	445	13 Q9B841 anguilla an
10	528	23.0	446	13 Q42315 cyprinus ca
11	525	22.9	385	5 Q24038 drosophila
12	524	22.9	437	13 Q42316 cyprinus ca
13	523.5	22.8	391	5 Q96716 brachistio
14	511.5	22.3	445	13 Q9B842 anguilla an
15	509	22.2	559	11 Q9QW71 rattus sp
16	503	21.9	399	5 Q9NG02 openg02 apis mellif
17	501	21.9	571	6 Q9FTM9 optm9 sus scrofa
18	496	21.6	448	13 Q9B844 anguilla an
19	493.5	21.5	477	5 Q9BM49

RESULT	1	SEQUENCE FROM N.A.
063004	PRELIMINARY;	PRY; 438 AA.
ID	Q63004	
AC	Q63004;	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)
DE	5-HT6 SEROTONIN RECEPTOR.	
OS	Rattus norvegicus (RAT).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCI-TAXID=10116;	
RP	[1]	
RC	SEQUENCE FROM N.A.	
RC	STRAINS-SPRAGUE-DAWLEY: TISSUE=BRAIN STRIATUM;	
RX	MEDLINE=96102917; PubMed=8222988;	
RA	Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Iachowicz J.E., Meitzer H.Y., Sibley D.R., Roth B.L., Hamblin M.W.;	
RT	"Cloning, characterization, and chromosomal localization of a human 5-HT6 serotonin receptor";	
RL	J. Neurochem. 66:47-55(1996).	
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL: L41146; AAC92633.1; -	
DR	InterPro: IPR00216; GPCR_Rhodopsn.	
DR	PFAM: PF00001; 7tm_1; 1.	
DR	PRINTS: PR00237; GPCRRHODOPSN.	
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL1_1; 1.	
DR	PROSITE: PS00262; G-PROTEIN RECEP_FL1_2; 1.	
KW	G-protein coupled receptor; Glycoprotein; Transmembrane.	
SEQUENCE	438 AA; 46786 MW; DB94043892F691A9 CRC64;	
Query	Match Best Local Similarity 88.4%; Score 2025; DB 11; Length 438;	
Matches	391;保守性 88.9%; Pred. No. 4-3e-136; Indels 35; Mismatches 12; Gaps 2;	
QY	1 MVPEPGPTANSTPAWGAGPPSAPGGSGWVAALCVVIALTAANSLLIAICIQPALRNT 60	
Db	1 MVPEPGPVNSSTPAWGAGPPSAPGGSGWVAALCVVIALTAANSLLIAICIQPALRNT 60	
QY	61 SNFLVLSEFTSDLMVGUVMPAPMLNALYGRMLARGLCLLWTFDVCMCSA1LNLCII 120	

```

: Db 61 |||||||SNFLVSLFTSDLMGLVYMPAMLNALYGRWLMQFDMCCSASILNCL 120
: Db 121 ||||DRYLILSPRLSPRYKLRRMPLRALARLVLGANSIALASFLPLIGWELGHARRPPVGQC 180
: Db 121 ||||DRYLILSPRLSPRYKLRRMPLRALARLVLGANSIALASFLPLIGWELGHARRPPVGQC 180
: Qy 181 RLLASLPFLVYASGLATFLPSGAICFYCRILLARKOAVQAVASLTGMSAQSETLQVP 240
: Qy 181 RLLASLPFLVYASGLATFLPSGAICFYCRILLARKOAVQAVASLTGMSAQSETLQVP 240
: Db 181 RLLASLPFLVYASGLATFLPSGAICFYCRILLARKOAVQAVASLTGMSAQSETLQVP 240
: Qy 241 RPPRGYESAASRRLAKTHSKRAKAKLTGILGMEFTWLFPEVANIVQAVCDQISPG 300
: Qy 241 RPPRGYESAASRRLAKTHSKRAKAKLTGILGMEFTWLFPEVANIVQAVCDQISPG 300
: Db 241 RPPRGMESADSRSRRLAKHSRKALKLTGILGMEFTWLFPEVANIVQAVCDQISPG 300
: Qy 301 LFDWLTLWLGNCNSTMDIYIPFMDFDKRFLGFLPQRCRERQASLSLRTSHSGP 360
: Qy 301 LFDWLTLWLGNCNSTMDIYIPFMDFDKRFLGFLPQRCRERQASLSLRTSHSGP 360
: Db 301 LFDWLTLWLGNCNSTMDIYIPFMDFDKRFLGFLPQRCRERQASLSLRTSHSGP 360
: Qy 361 RGGGLSQQQLPPLPPDSDSDAGSGGSSGLRLLTAQOLLGEATODPPLTRAAVN 420
: Qy 361 RGGGLSQQQLPPLPPDSDSDAGSGGSSGLRLLTAQOLLGEATODPPLTRAAVN 420
: Db 361 RGGGLSQQQLPPLPPDSDSDS--ASGGTSQLQTAOLULLPGEATRODPPTTATTVNF 418
: Qy 421 FNIDPAPPELPHPLGIGPTN 440
: Qy 421 FNIDPAPPELPHPLGIGPTN 440
: Db 419 FVTDSVEPEIREHPLSPVN 438

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RESULT

2

PRELIMINARY;

PRT; 405 AA.

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: Db 09CRR2 |||||||O9CRR2; PRELIMINARY; PRT; 405 AA.
: Q9CRR2; PRELIMINARY; PRT; 405 AA.
: Ac_ DT 01-JUN-2001 (TREMBLrel. 17, Created)
: Dt 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
: Dt 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
: De ADRENERGIC RECEPTOR, BETA 1 (FRAGMENT)
: Gm ADRBL1
: Os MUS musculus (Mouse).
: Oc Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
: Oc Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
: Ox NCBI_TaxID=10090;
: Rn [1] SEQUENCE FROM N.A.
: Rn STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;
: Rx MEDLINE=21085660; PubMed=11217851;
: Ra Kawai J., Shingawa A., Shiba K., Yoshino M., Itoh M., Ishii Y.,
: Ra Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Yamamoto I.,
: Ra Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Kasukawa T., Saito T.,
: Ra Saito T., Okaaki T., Gojobori T., Bono H., Kasukawa T., Saito R.,
: Ra Kadota K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T.,
: Ra Fleischmann W., Gaasterland T., Glissi C., King B., Kochina H.,
: Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quakkenbush J.,
: Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
: Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
: Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
: Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
: Ra Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
: Ra Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
: Ra Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
: Ra Suzuki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
: Ra Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
: Ra Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."
: Rl Nature 409:685-690(2001).
: Cc -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
: Cc -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
: Dr EMBL: AK018378; BAB31185.1; -
: Dr MGD: MG1:87937; Adrb1.
: Dr InterPro: IPR000276; GPCR_Rhodopsn.
: Dr Pfam: PF00001; 7tm_1; 1.
: Dr Prints: PR00237; GPERRHODOPSN.
: Dr PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
: Dr PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
: Dr G_protein_coupled_receptor; Glycoprotein_Receptor; Transmembrane.
: Sq SEQUENCE 405 AA; 42886 MW; EF4B13BB413EA413 CRC64;

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RESULT

3

PRELIMINARY;

PRT; 405 AA.

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: Db 09GL56 |||||||O9GL56; PRELIMINARY; PRT; 405 AA.
: Q9GL56; PRELIMINARY; PRT; 405 AA.
: Ac_ DT 01-MAR-2001 (TREMBLrel. 16, Created)
: Dt 01-JUN-2001 (TREMBLrel. 15, Last sequence update)
: Dt 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
: De B3AR. ADRENERGIC RECEPTOR.
: Gm OS Ovis aries (Sheep).
: Gm OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
: Gm OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
: Gm OC Bovidae; Caprinae; Ovis.
: Gm OC NCBI_TaxID=9940;
: Rn [1] SEQUENCE FROM N.A.
: Ra Forrest R.H., Hickford J.G.H.; "Polymorphism within the ovine beta 3 adrenergic receptor gene."
: Rt -!- Submitted (OCT 2000) to the EMBL/GenBank/DBP databases.
: Rl CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
: Rl CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
: Dr EMBL: AF314203; AAC31166.1; -
: Dr InterPro: IPR000276; GPCR_Rhodopsn.
: Dr Pfam: PF00001; 7tm_1; 1.
: Dr Prints: PR00237; GPERRHODOPSN.
: Dr PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
: Dr PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
: Dr G_protein_coupled_receptor; Glycoprotein_Receptor; Transmembrane.
: Sq SEQUENCE 405 AA; 42886 MW; EF4B13BB413EA413 CRC64;

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Query Match

25.2%

Score 578;

DB 11;

Length 405;

DB 11;

Db	131	LAVDRYLAVINPRLIGALVNRKARRAVALVWVSAVSFAPMSKWWVGADAEQRCR	190	Db	248	EESPAPASRSQSPGPAG---PYASPVGVPSYGRPARLPLREIRAR---TIGLIMG	299
Qy	172	ARPVPVGQCRLLASLFLFVFLVAGSLTFLPLSACIFCYCRLLAARRQAV-----	222	Qy	276	MFFVTWLFPEFVANIQAV---CDC1SPLGLFDVLTLWLGVCNSTMNPITY--PLFMRDFKRA	330
Db	191	SNPRC--CTPFASSNMYPALISSSVSYLPLVMFLFYARFVVATQQLRURRLERGRFP	247	Db	300	TFTLCWLWPFVNWNVRALGGPSLVSQGPTFLALNWLGYANSAFNPLYCRSP---DFRSA	355
Qy	223	--ASLTIGMASQASETQVPRTRPRGYESADSR--RLATHSKAKLAKTIGLG	275	Qy	331	LGRLFLCPCCRER-----QASLASPRTSHSGPRGSPLSIQVLPULPPSDSDS	382
Db	248	EESPAPASRSQSPGPAG---PYASPVGVPSYGRPARLPLREIRAR---TIGLIMG	299	Db	356	FRLL-C-RCPEEHAAASP---PRAPSGAPTIVLSPAGPRQSPLDGASCGLS	397
Qy	276	MFFVWVILPFFVANIQAV---CDC1SPLGLFDVLTLWLGVCNSTMNPITY--PLFMRDFKRA	330	Qy	383	DAGGGSSGL	392
Db	300	TFTLCWLWPFVNWNVRALGGPSLVSQGPTFLALNWLGYANSAFNPLYCRSP---DERSA	355	Db	398	---DGASGL	404
Qy	331	LGRLFLCPCCRERQASLASPRTSHSGPRGSPLSIQVLPULPPSDSDS	390	RESULT	7		
Db	356	FRLL-C-RCPEEHAAASP---PRAPSGAPTIVLSPAGPRQSPLDGASCGLS	395	ID	044198	PRELIMINARY;	PRT; 402 AA.
Q9GL57	09GL57	PRELIMINARY;	PRT; 405 AA.	ID	044198	PRELIMINARY;	PRT; 402 AA.
AC	09GL57;			AC	044198;		
DT	01-MAR-2001 (TREMBrel. 16, Created)			DT	01-JUN-1998 (TREMBrel. 05, Created)		
DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)			DT	01-JUN-1998 (TREMBrel. 06, Last sequence update)		
DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)			DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)		
DE	BETA 3 ADRENERGIC RECEPTOR.			DE	DOPAMINE RECEPTOR, D1.		
GN	B3AR.			GN	DOP1.		
OS	Ovis aries (Sheep)			OS	Apis mellifera (Honeybee).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.			OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apidae; Apis.		
OX	NCBI_TAXID=9940;			OX	NCBI_TAXID=7460;		
RP	SEQUENCE FROM N.A.			RP	[1]		
RA	Forrest, R.H.; Hickford, J.G.H.;			RA	SEQUENCE FROM N.A.		
RT	"Polymorphism within the ovine beta 3 adrenergic receptor gene."			RA	Baumann A.;		
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.		
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
EMBL	AF314200; AAQ31163.1;			EMBL	Y13429; CAJ73841.1;		
DR	INTERPRO: IPR000276; GPCR_Rhodpsn.			DR	INTERPRO: IPR000276; GPCR_Rhodpsn.		
DR	PFAM: PF00001; 7tm_1.			DR	PFAM: PF00001; 7tm_1.		
DR	PRINTS: PR00237; GPCR_Rhodpsn.			DR	PRINTS: PR00237; G-PROTEIN_RECEP_FL_1; 1.		
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL_2; 1.			DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL_2; 1.		
DR	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.			DR	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.		
KW	SEQUENCE 405 AA; 42928 MW; 6C9B1EBBF90F54B CRC64;			KW	SEQUENCE 402 AA; 44554 MW; OB1962DC7F6481DF CRC64;		
SQ				Query Match	23.8%	Score 546.5; DB 5; Length 402;	
				Best Local Similarity	36.4%	Pred. No. 2_6e-31;	
				Matches	133;	Conservative 55; Mismatches 146; Indels 31; Gaps 7;	
				Matches	133;	Best Local Similarity 34.0%; Pred. No. 5_7e-32;	
				Matches	146;	Conservative 59; Mismatches 151; Indels 74; Gaps 15;	
Query	1	MVPEPG-PTANSTPANGAGPSSAPGCGSGWVAALCVVIAVTAANASNLIALCTOPALRN	59	Qy	35	VVITALTAANASNLIALCTOPALRNTSNFLVSLFNSDLWMLGVLVAPPAMINALGRWVL	94
Db	11	LTPWPDIPTLAPNTANASGLFGFVPAVALAGALLALAVLATVFGNLEVIVAIAPRPLQ	70	Db	34	IILFLSVAGNLVCAVYTDRGLRIGNLFLASLATADLFVGLVMTFAGVNDLGLGYWF	93
Qy	60	TSNFEFLVSLFSDLMGLVNVMPAMINALGRWVLARGICLWTARDVDMCCSASTLNCL	119	Qy	95	ARGCLLIWTADPVMCCSASTLNCLISLDRLVLLSPRLYKRMPLRFLALVLGWSIA	154
Db	71	MTNFVFTSLATADLVVLLVVFATLGTCHWPLGVTCVGCETWTSVDBLCVTAETLCA	130	Db	94	GPRFCDTWIAFDVMCSTASTLNCLISLDRLYTHIKDPLVGRWVTRRIAVAGIAVWLLA	153
Qy	120	ISLDRLLLILSPRLYKRMPLRFLALVLGWSIAASLFLPLLGWHLG-----H	171	Qy	155	ALASFPLLGLLGHARV-----PGQCLLPLASPLVFLVAGLTFPLPSGAICF	206
Db	131	LAUDRYLAVINPRLIGALVNRKARRAVALVWVSAVSFAPMSKWWVGADAEQRCR	190	Db	154	GLISFVPISLGH--RANEPVFLDSDKEEHTCAALDTPIYAVISSISFVPCVMLG	210
Qy	172	ARPVPVGQCRLLASLFLFVFLVAGSLTFLPLSACIFCYCRLLAARRQAV-----	222	Qy	207	TYCRLLAARRQAVQYASLT---TOMASQASETQVPRTRPRGYESADSR LATHSRK	262
Db	191	SNPRC--CTPFASSNMYPALISSSVSYLPLVMFLFYARFVVATQQLRURRLERGRFP	247	Db	211	IYCRLCYAQKHKVSKTRAVTKLDPDSMAKSFKVHKATPKPQTKI--KPTSPYHVS	266
Qy	223	---ASLTIGMASQASETQVPRTRPRGYESADSR--RLATHSKAKLAKTIGLG	275	Qy	263	ALKAKLTLGTLGFMFVWLFPEFVANIQAVC--DC1SPGLFLDVTLWLGVCNSTMNPITY	321
Db				Db	267	DHKAAITVGVINGVFLCWCWVPCFCVNUTSYCKTCISGRAFOVLTWLGYSNSAFNPYI	326
Qy				Qy	322	LFRMDKRALGRFLCPRCRPRQASLASPLSRTSHSGPRGSLQO--VLPFLPPD	377
Db				Db	327	INTEFRAEKRILKGARANGNPS----TSCGEFRSYWVVKRNSMIECNISPR	379

QY 378 SDSDS 382 PRELIMINARY; PRF; 445 AA.
 ID Q9M200 ID:II
 AC Q9B841;
 DB 380 SSADS 384 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE B7E-A-3 ADRENERGIC RECEPTOR.
 OS SUS scrofa (Pig).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBITaxID=9823;
 RN [1] SEQUENCE FROM N.A.
 RP Smith T.R., Bidwell C.A., Mills S.E.;
 RA "Sus scrofa beta-3-adrenergic receptor (BAR3) gene."
 RT Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 RL -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF274007; RAEF2301_1; -
 DR InterPro: IPR00216; GPCR_Rhodpsn.
 DR Pfam: PF0001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 407 AA; 43610 MW; C6598382A9B38DD9 CRC64;

Query Match 23.6%; Score 540.5; DB 6; Length 407;
 Best Local Similarity 33.0%; Pred. No. 7.1e-31; Indels 85; Gaps 15;
 Matches 146; Conservative 55; Mismatches 157; RT
 RT
 QY 5 PGSTANST-----PAWAGAGPSAPCGSCGWAAALCWCWITALTAANSLILLI 51
 DR 3 PWQOGNSSLPPRDPVSTLAPNNNTSGLPGVPVALAGALLAPAVLATVGGLNLIVAI 62
 QY 52 CTPPALRTSNEFLVLSIFTSDDNGVLYWMPAMLNALYGRWYLARGCQLLWPAFDWMC 111
 DR 63 ARTPLQMTNVFTSLATADLVGLVLLVPPGTTLALGHWPAGTCELWISVDLVCVT 122
 QY 112 ASILNLCLISDRYLLSPRYKLRLMPRLRALVLGAWSLAALASFLPLLGWHELG- 170
 DR 123 ASIETLCLALAVDRLYLAVINPRLRGALVYKRRARAAVVLWVVAASFAPTMKWVRGA 182
 QY 171 -----HARPPVPGOCRLLASIFPVLYASGLTFFLPSGACTTYCRTLAAARKQ---A 219
 DR 183 DAEAQORCHSNPSC--GTFASNMPYALSSVSYFLPLVLMLEVARYRVFWVATSQLRLR 239
 QY 220 VVAVSLTGMAQSASETLQVPRPP---GYESADSR--RKAATKHSRKAKAKLULGI 272
 DR 240 WEISRFPEEPSPAPSRSQSPAPGRPNWPSAGVPHGRPARLPLREHRL--CWLGL 296
 QY 273 LIGGMFFVWLPFPEVANTVQAVCDCISPL---FDVLTWLGYNSTMNPPIYPLFMRDF 327
 DR 297 IMGTFLCWLPLPFVWNVVRAKG---GOSLVPVPAFLAINWLGYAANSAENPLY-chSPDF 352
 QY 328 KRALGRFLPCPQPRERORASLASSPLSLQQLVPLPLPPDSDDSDAGSG 387 PRELIMINARY; PRF; 446 AA.
 DR 353 RSAFRLL-C-RGCPEEHLAAMSP----PR----APSG 380 042315 ID:II
 QY 388 GSSGLRLTAQOLLPGEAOTDPP 410 042315 ID:II
 DR 381 APE-----TLTHPAESRQSPPL 397 042315 ID:II
 RESULT 8 ID:II
 ID Q9M200 PRELIMINARY; PRF; 407 AA.
 AC Q9B841;
 DB 380 SSADS 384 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE DOPAMINE DIA1 RECEPTOR.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE:9716083; PubMed:9006917;
 RA Cardinaud B., Coudouel S., Vincent J.-P., Vernier P.;
 RT "Early emergence of three dopamine D1 receptor subtypes in European eel Anguilla anguilla.", J. Biol. Chem. 272:2778-2787(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: U02918; AAC0067.1; -
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF0001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 445 AA; 49442 MW; 2426D945DE39ACDD CRC64;

Query Match 23.3%; Score 535; DB 13; Length 445;
 Best Local Similarity 35.4%; Pred. No. 1.9e-30; Indels 30; Gaps 7;
 Matches 116; Conservative 61; Mismatches 121; RT
 RT
 QY 33 LCWVIALTAANSLILACITOPALRN-TSNFLVSLFTSDLMGLVWMPAMLNALYGR 91
 DR 28 LSLILITLPLGNLNTCAAVTRFRHLRSKVNFVILSILSLLVAILVWMPWKATEIVGF 87
 QY 92 WLIARGLCILWTAIDVDMCCSASTINLCLISDRYLLISPLRYKLRLMPRLRALVLGWA 151
 DR 88 WPFG-SFCMWVAFDINGSTASILNLCVSVDRWIALSSPPFRYERKMFPPKVAFWMSVW 146
 QY 152 SLAALASEDPLLGWHELGA-----RPPVPGCRLIASLPFWVIAWSGLTFFES 201
 DR 147 TLSVLISFPLVQVOLWPKHQAGFPFELNGTFREPPIPDDNSLRNTYIASLISLYFV 206
 QY 202 GAICFTYCRLLAARKQAOVQAVASLTGMSAQASETLOVERTPRPGVESADSRRLATKHSR 261
 DR 207 AIMVUTVPTYRQAQKQIRISALERAARSAKNRHSMNS---IFESSFSRMSFKRET 262
 QY 262 KALKAKLTGIGLGMFFVWLPFPEVANTVQAVCD-----CISRLDFVLTWLGYC 311
 DR 263 KVLR---TLSVIMGVFWCQWLPLFFILNCMVNPFCQAOQGAIDLPCVSSITFDFVFWFGWA 319
 QY 312 NSTMNPIYPLFEMDFKRNLGRELPCP 339
 DR 320 NSSNPIYI-ANFADFRKFATSTLGCHR 346
 RESULT 10 ID:II
 ID O42315 PRELIMINARY; PRF; 446 AA.
 AC 042315 ID:II
 DR 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE DIA3 DOPAMINE RECEPTOR.
 OS Cyprinus carpio (Common carp).
 OC Cypriotes carpio (Common carp); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

RESULT 9 ID:II
 ID 098841 PRELIMINARY; PRF; 445 AA.
 AC 098841;
 DB 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE DIA1 DIA1 RECEPTOR.

Db	147 TLLSLISIPIPVOLANWIKAQTTISFDHNSYGDLLNDQDSSLNRTYAISSSLISFYIPVA	206	QY	336 PCRCPRPRQA-SLASI--SL-----RTSHSGPR-----PGLSIQQVILPLP	373
OY	203 ATCCFTCIRLLARKQAVQAVASITGMASQASETLQLQPRTRPRGVESADSRLATKHSRK	262	Db	412 RC-OCRRRRRRLRPLASLDRRAFRRLRPOPSSRSRGPPSSPHCTPGCLGLR----	465
Db	207 IMIVTYTRIYRINKQIRRISALE--RAESEAKRNHNSMGNSMSSVETESSFKMSKRRET	264	QY	374 LPPDSDSADAGSG--GSSGURLTAQOLL	400
OY	263 AIKAKTGLSILGMFFVWLPLPFVANIVQAVD-----CISPLGLFVLWTWIGYC	311	Db	466 -----HAGDAGFGLQOSKASLRLREWRLL	489
Db	265 VLK--TLSVINGEVFCWLPLPFILNCMVPCQAHNGSADFPVCVSSTTFNWFWFGWA	321	QY	312 NSTMNPIYPFLMDKFRLGRFLPCPR-CPRQRQASLASPLRTSHSGPRGL	364
OY	322 NSSLNPIY-RPNDFKKAFAKSLLGCRICPQSSNATEIVS---INNNGAPPOL	370	Db	322 NSSLNPIY-RPNDFKKAFAKSLLGCRICPQSSNATEIVS---INNNGAPPOL	370
RESULT	15				
O9QW71					
ID	090W71	PRELIMINARY;	PRT;	559 AA.	
AC	09QW71;				
QT	01-MAY-2000 (TREMBrel. 13, Created)				
DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)				
DE	ALPHA 1-ADRENERGIC RECEPTOR SUBTYPE ALPHA 1D, ALPHA 1D-AR.				
OS	Rattus sp.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
NCBI_TAXID	10118;				
OX	[1]				
RN					
RP	SEQUENCE FROM N.A.				
RX					
RA	MEDLINE=92100054; PubMed=1661838;				
RP	"Solution-phase library screening for the identification of rare clones: isolation of an alpha 1D-adrenergic receptor cDNA.",				
RT	Mol. Pharmacol. 40:876-883(1991).				
RL	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	Interpro: IPR000276; GPCR_Rhodopsin.				
DR	Pfam: PF00001; 7tm_1, 1.				
DR	PRINTS: PR00237; GPCRHHODPSN.				
DR	PROSITE: PS50262; G_PROTEIN_RECEP_FL_2; 1.				
DR	G-protein coupled receptor; Glycoprotein; Transmembrane-SEQUENCE				
SO	559 AA; 59739 MW; 37C9BD666D3A47D CTC64;				

Query Match 22-28; Score 509.5; DB 11; Length 559;
 Best Local Similarity 33.3%; Pred. No. 1.5e-28;
 Matches 150; Conservative 63; Mismatches 158; Indels 79; Gaps 19;

QY	4 EPGPIA---NSTPAWGAGPSA-PG-GSGWVAALCWVIAITAANSLLTL-ICTQPAL	57
Db	66 EPGAAAGSEGVNGSAVVGGLVVA-SQGVGVYFLA---FILTAVAGNLVLTSVACNRHL	121
QY	58 RNTSNFLVSLFSTDLMVGLVMPAMNLAYGRWVLARGICLTWTAFDYMCCCASILNL	117
Db	122 QTVTWVFIVNLAVADLLSAAVPLPSATMEVIGWAFGRIFCDWVAVDLCCTASILSL	181
QY	118 CLISIDRYYLILSPRLYKLRMLPALARLVAGWAAALASFLPLIGWELGHARPPVP	177
Db	182 CTISVDRYVGVRHSLKYPAIMIERKAATLALLAWVALVVSVGP-LIGWKE----PVP	234
QY	178 GQ--CRLLASLPFVLVASGLTFLPSGAICFTCIRLLARKQAVQAVASITGMASQAS	234
Db	235 PDERFCGITEEVGYAIFSSVCSVFLPMAVTVVMCYVWRS---TTRSLEAGIKREGP	291
QY	235 ETLQV-----PRTPR -- PGVESADSRRLATKHSRKL----KAKLTG3TLLGMF	277
Db	292 KASEVVLRHCGRAGTSAKGYPGROSSKGHTLRSLSVLKFREKAKTTLAIWGVF	351
OY	278 FVTWLFPEFFVANIIVQAVCDCISP-GLFDVLTWLGYCNSTNPITYPLFMRDFKRALGREL	335
Db	352 VLCWPFPFFVPLPLGSISIPOKPSSEGKVIVLWLYFNCSVNPLYPCCSSREFKAFRL	411

Search completed: March 15, 2002, 14:14:05
 Job time: 211 sec

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Om protein - protein search, using sw model

Run on: March 15, 2002, 14:08:30 ; Search time 14.43 Seconds

(without alignments)
686.171 Million cell updates/sec

Title: US-09-826-509-449

Perfect score: 2292

Sequence: 1 MVPEPGPTANSTPAWGAGPP..... FNIDPAEPELRLRPHPLGPTN 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cggn_2_6/ptodata/2/1aa/5A_COMB_pep: *
 2: /cggn_2_6/ptodata/2/1aa/5B_COMB_pep: *
 3: /cggn_2_6/ptodata/2/1aa/6A_COMB_pep: *
 4: /cggn_2_6/ptodata/2/1aa/6B_COMB_pep: *
 5: /cggn_2_6/ptodata/2/1aa/PCRTUS_COMBO_pep: *
 6: /cggn_2_6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	55.7	24.3	468	2 US-08-390-000A-7
2	55.7	24.3	477	1 US-08-087-772A-16
3	55.4	24.2	405	1 US-08-351-73B-2
4	55.3	24.1	365	2 US-08-467-559B-9
5	55.2	24.1	400	1 US-08-351-473B-5
6	55.2	24.1	400	4 US-08-450-982-4
7	55.2	24.1	400	4 US-08-450-982-6
8	55.2	24.1	446	1 US-07-626-638A-21
9	552.5	24.1	446	1 US-08-333-977-21
10	551.5	24.1	400	1 US-07-916-901-6
11	551.5	24.1	400	1 US-07-783-602C-1
12	551.5	24.1	400	1 US-08-351-473B-4
13	55.1	24.1	477	1 US-08-44-73A-4
14	54.7	23.9	446	2 US-07-969-267B-4
15	54.6	23.8	388	1 US-08-087-772A-2
16	53.5	23.5	472	1 US-08-194-33A-6
17	53.5	23.3	487	1 US-08-44-473B-3
18	53.3	23.3	408	1 US-08-351-473B-3
19	53.1	23.2	402	1 US-08-44-73A-6
20	53.1	23.2	402	1 US-08-087-772A-15
21	53.1	23.2	408	1 US-07-916-901-2
22	53.1	23.2	408	4 US-08-450-982-2
23	53.1	23.2	408	4 US-08-450-982-5
24	52.4	22.9	446	1 US-07-626-618A-22
25	52.4	22.9	446	1 US-08-333-977-22
26	52.3	22.8	400	2 US-08-103-170-9
27	51.5	22.5	483	1 US-08-194-338-7

RESULT 1
US-08-390-000A-7
; Sequence 7, Application US/08390000A
; Patent No. 5985583
GENERAL INFORMATION:
; APPLICANT: Sealton, Stuart C.
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,000A
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
; NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6923-052
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-390-000A-7
Query Match Best Local Similarity 24.3%; Score 557; DB 2; Length 468;
Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;
Oy 1 MVPEPGPTANSTPAWGAGPPSAPGGSGWVAAACVVLTAANSLIACTQPALNT 60
Db 24 LVPASPPASLPPASESPPELPSQQWAGMGLMLAVLVLIVAGNVIVVAKTRQLQ 83

Query Match 24, 3%; Score 557; DB 1; Length 477;
Best Local Similarity 33.8%; Pred. No. 9.2e-35; Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;

QY 61 SNNFLVSLFSTDIAVGLVYMPAMLNAYGRWVLARGICLLWPAFDWMCASILNLCI 120
Db 84 TNLFIMSLASADLVMGLLVPGFTIVWGRWEYGSFFCELMWTSVDLVCVTASIELCWI 143

QY 121 SLDRYLILISPLRKYKLRMPLRLALVLGAWSLAALASFLPLLGW- HELGHARPPV- 176
Db 144 ALDRLYLATISPLRKYQSLULTRARAGLVCYWAISALVSFLPLTMHWWRAESDEARRCYND 203

QY 177 PGOCRLLASLPFVIVASGLTFLFELSGATTCFTYCRILLAARKQAVQVAS--- LTIGMASQ 232
Db 204 PKCCDFVTRAYAASSVSVFVPLCIMAFVYLRVRFREAQOKQKKIDSERRFLGGPAPR 263

QY 233 ASET-----LQVPTPRGVESADS-----RLATKHSRKALKAKLTGIL 273
Db 264 PSPPSPSPVAPAPPGPGRPPRAAAATAPLANGRAGKRRPSRLVALREOKALK--TGLII 320

QY 274 LGMFVUTWLPFVIVANIVQAV-CDCISPLGFEDVITWLGCNSTNPIV-- PLEMDKRR 329
Db 321 MGVFTLCLWLPFELANVVKFHRELVPDRLFVFFNWLGYANSAENPNTIVCRSP---DFRK 376

QY 330 ALGRFLPCRCPRQRQASLASPLSRTSHSGPROGLSLOQVLPFLP- PDSDSDAGSGG 388
Db 377 AFQGLLCCARRAARRHATHGDRPRASGCLARP-----PPSPGAASDDDDDVWGA 429

QY 389 SSGRL 394
Db 430 TPPARL 435

RESULT 2

US-08-087-772A-16
Sequence 16 Application US/08087772A
Patent No. 5691155

GENERAL INFORMATION:

APPLICANT: Nahmas, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.

TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine Beta3-Adrenergic Receptor and Their Applications

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linter, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-087-772A-16

RESULT 3

US 08-351-473B-2
Sequence 2, Application US/08351473B
Patent No. 565640

GENERAL INFORMATION:

APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBON, SPVAK, MCLELLAND, MATER & NEUSTADT
STREET: 175 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-OX PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 405 amino acids

TYPE: amino acid

TOPOLGY: linear

MOLECULE TYPE: protein

US-08-351-473B-2

Query Match 24.2%; Score 554; DB 1; Length 405;

Best Local Similarity 33.6%; Pred. No. 1. 3e-34; Mismatches 156; Indels 66; Gaps 13; Matches 143; Conservative 61; MisMatches 156; Indels 66; Gaps 13;

QY 1 MVPEPG-PTANSTPAWGAGPPSAPGSGWVAAICVVIATTAANSLLALICTOPALRN 59

Db 11 LTPWPWDIPTIAPNTANASGLPGVPAVALAGALLAVALATVGNNLIVTAVATPRPLQT 70

QY 60 TSNFELFLSFLISDMLVGLVMPAMLNLYGRWVLARGCLLWAFDVWCGSASILNCL 119

Db 71 MTNVEVTSLATPADLVGLVYPPGATLATHGWPIGVTGEGELMTWSDVLCVTAIETICA 130

QY 120 ISLDRLVLLSPRYKLRTPLRALTALVIGAWSALASFLPLLGWHEG-----H 171

Db 131 LAVDRLAVINPLRGALVKKRALAAVVLWVNNSAVSFAPIMSKWWRIGADAEORCH 190

QY 172 ARPPVPGQCRLLASIFVFLVAVASGLLFPLPSGAICFTYCRILLAARKAQAVASYLTGM-- 229

Db 191 SNPRC---CTPASNPYALSSSSVSPYPLVLMFLVYARVVFVATRQ-LRLRLRELGFP 246

QY 230 -----ASQASETILQVPRIPRPGVESADSR--RLAKTHSKRAKAKLTGIGLGMFV 279

Db 247 PEESPPAPSRSGGIAGPASPAGPSYKSRPPLBHRAR--TGLGIMGTEFL 303

QY 280 TWLPLPFVANTVQAV--CDCITSPGLFDVLTLWGLYCNCSTMNPIY--PLFMRDFRKLGRF 334

Db 304 CWLPLPFVNVNVRALAGGSPSLVSGPTFLALNLNGYANSAFNPLIYCRSPDPFRSAFRRLCRC 363

QY 335 LP-----CPCRCRERQASLASPLSLRTSHSGPRRGLSFOQVLLPLRPPDSDSDAGS 386

Db 364 RPEEHLLAASPPRAPS-----GAPITALTSPAGPMO-----PELD----- 398

QY 387 GGSGL 392

Db 399 GASCGL 404

RESULT 4
US-08-467-559B-9

; Sequence 9, Application US/08467-559B

; Patent No. 5528890

GENERAL INFORMATION:

; APPLICANT: LI, TI

; TITLE OF INVENTION: HUMAN AMINE RECEPTOR

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STEINE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 20005-5934

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/467-559B

; FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SIEFFE, ERIC K

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0840000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2500

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 365 amino acids

TYPE: amino acid

STRANEDNESS: not relevant

MOLECULE TYPE: protein

US-08-467-559B-9

Query Match 24.1%; Score 553.5; DB 2; Length 365;

Best Local Similarity 37.8%; Pred. No. 1. 3e-34; Mismatches 134; Indels 35; Gaps 12; Matches 137; Conservative 56; MisMatches 134; Indels 35; Gaps 12;

QY 7 PTANSTPAWGAGPPSAPGGSGWVAAICVVIATTAANSLLALICTOPAI.RNTSINF 63

Db 9 PPASLIPPASEG---SAPLSQWWTAGKGMLLAVLIVLIVGVNLVWVAKTRPLQLTN 66

Qy 64 FLVSILFTSDMLVGLVMPAMLNLYGRWVLARGCLLWAFDVWCGSASILNCLSID 123

Db 67 FIMSLASADIYLMLVGLLVPGFATIVVWGRWEYGSEFCELWTSVDLVCVTAIETICVIALD 126

Qy 124 RYLLTISPLRYKLRTPLRALTALVIGAWSALASFLPLLGW--HELGHARPY--PGO 179

Db 127 RYLAITSPLFRQSLUTRARALARVCLWVWASALSVPLMHWRAESDIBARRCYNDPKC 186

Qy 180 CRLLASLPVIVAVASGLTFEPGATCFTYCRILLAARKAVOVA-----LTTGMAOSA- 234

Db 187 CDFVTRNAYIAASSVSVFYPLCIMAFVYLVFREAKOKKIDSCCRKLGGPAPRPS 246

Qy 235 ETLQVTRTPRPGVESADSR-----RLAKTHSKRAKAKLTGIGLGMFVWTWPFVVA 287

Db 247 EPSPSPGPPIPRAFDLSLANGRSKRRPSRLVLAUREQKALK--TGLGIMGVTLCLWPLFFLA 303

Qy 288 NIVQAV-CDCTISPLGFEDVLTLWGLYCNCSTMNPIY--PLFMRDFRKLGRFPCR--C 340

Db 304 NVVKAHRDLVPDFRLEVFNWLNGYANSAFNPLIYCRSP---DERKAQORLCCARRAAC 359

Qy 341 PR 342

Db 360 RR 361

RESULT 5

US-08-351-473B-5

; Sequence 5, Application US/08351-473B

; Patent No. 556440

GENERAL INFORMATION:

; APPLICANT: LEZENZ, GERLINDA

; APPLICANT: KAPOOR, ARCHANA

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE

; TITLE OF INVENTION: BOVINE BETA-3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: USA

; ZIPL: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/351,473B

FILING DATE: 21-FEB-1995

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 93 04670

FILING DATE: 21-APR-1993

PRIORITY APPLICATION DATA: PCT/FR94/00447

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 6639-001-0X PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248655 OFPAT UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-351-473B-5

Query Match 24.1%; Score 552.5; DB 1; Length 400; Best Local Similarity 35.1%; Pred. No. 1.7e-34; Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

QY 5 PGPTANSTPA-WGAGP--PSAPGGSG---WVAALCVVIAL-TAANSLILALICTQ 54

Db 3 PWPHRNGSLALWSDAPTLDPSSAANTSGLPGVPWAALAGALLATVGNLVLVIAART 62

QY 55 PALRNTSNFLSFLTSIDLWGLVMPAMNLAYGRWLARGLCILWTAFDWMCASAI 114

Db 63 PRQQTINVTFTSLAADIVVGLLVMPPGATLALTGHPLGECELMWSVDLVCVTASI 122

QY 115 LNCLCLISDRLYLILTSPLRYKLRLMPLRALAVLGAWSLAALASFPLPLLGWHELG--- 170

Db 123 ETLCALAVDRLYLVNPLRYGLTWRKRAARAVLVWVVIASAASFAPIMSQWRVGDAE 182

QY 171 ---HARPPVPGQCCRLLASLPFLVIVASGLTFFESGACITFCYRILLARKQAVQVASLT 226

Db 183 AQECHSNPRC--CSFASNMPYALLSSSVSYFPLVMLFVAVRVVAKOR-HLRR 238

QY 227 TGMSAQASETLQLQVTPRTPR-----GVEASDR--RLATKHSRKALKLTGILL 274

Db 239 LGFSPESPSSPPSPSRSPATGGTAAPDGVPPGCRARRPLPREHRLR--TLGLIM 295

QY 275 GMFVTWLPFFVANIQAVC--DCISPGFLDVTLWLGICNSTMNPITY--PLFMDKFR 329

Db 329 GFSLCLWLFELVNLRAAGPSLVPSCVFIANWLGLFANSAPNPVYCRSPDFRDAFR 355

QY 330 AL---GRFLPCPRC--PRERGASLASPSLR--TSHSGPRP 362

Db 356 LLCSYGGRGPEEPRAVTFPASPVEAROSPPLNRFDGYEGARP 397

RESULT 6

US-08-450-962-4

Sequence 4, Application US/08450962

Patent No. 6274706

GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHN & CATE

STREET: P. O. BOX 06110

CITY: CHICAGO

STATE: ILLINOIS

COUNTRY: U.S.A.

ZIP: 60606-0110

COMPUTER READABLE FORM:

MEDIUM TYPE: 3-1/2" diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,962

FILING DATE:

CLASSIFICATION: 530

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/117,829

FILING DATE: 08-SEPT-1993

APPLICATION NUMBER: 07/721,571

FILING DATE: 25-MAY-1990

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/FR89/00918

FILING DATE: 25-JAN-1989

ATTORNEY/AGENT INFORMATION:

NAME: Fleit, Martin; Golin, Michael A.

REGISTRATION NUMBER: 16,900; 31,957

REFERENCE/DOCKET NUMBER: 47078-042

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 789-3400

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 residues

TYPE: amino acid

TOPOLOGY: linear

DESCRIPTION: polypeptide

US-08-450-962-4

Query Match 24.1%; Score 552.5; DB 4; Length 400; Best Local Similarity 35.1%; Pred. No. 1.7e-34; Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

QY 5 PGPTANSTPA-WGAGP--PSAPGGSG---WVAALCVVIAL-TAANSLILALICTQ 54

Db 3 PWPHRNGSLALWSDAPTLDPSSAANTSGLPGVPWAALAGALLATVGNLVLVIAART 62

QY 55 PALRNTSNFLSFLTSIDLWGLVMPAMNLAYGRWLARGLCILWTAFDWMCASAI 114

Db 63 PRQQTINVTFTSLAADIVVGLLVMPPGATLALTGHPLGECELMWSVDLVCVTASI 122

QY 115 LNCLCLISDRLYLILTSPLRYKLRLMPLRALAVLGAWSLAALASFPLPLLGWHELG--- 170

Db 123 ETLCALAVDRLYLVNPLRYGLTWRKRAARAVLVWVVIASAASFAPIMSQWRVGDAE 182

QY 171 ---HARPPVPGQCCRLLASLPFLVIVASGLTFFESGACITFCYRILLARKQAVQVASLT 226

Db 183 AQECHSNPRC--CSFASNMPYALLSSSVSYFPLVMLFVAVRVVAKOR-HLRR 238

QY 227 TGMSAQASETLQLQVTPRTPR-----GVEASDR--RLATKHSRKALKLTGILL 274

Db 239 LGFSPESPSSPPSPSRSPATGGTAAPDGVPPGCRARRPLPREHRLR--TLGLIM 295

QY 275 GMFVTWLPFFVANIQAVC--DCISPGFLDVTLWLGICNSTMNPITY--PLFMDKFR 329

Db 329 GFSLCLWLFELVNLRAAGPSLVPSCVFIANWLGLFANSAPNPVYCRSPDFRDAFR 355

QY 330 AL---GRFLPCPRC--PRERGASLASPSLR--TSHSGPRP 362

Db 356 LLCSYGGRGPEEPRAVTFPASPVEAROSPPLNRFDGYEGARP 397

RESULT 7

US-08-450-962-6

; Sequence 6, Application US/08450962

; Patent No. 6274706

; GENERAL INFORMATION:

; APPLICANT: EMORINE, Laurent; MARULLO, Stefano;

; TITLE OF INVENTION: INTRO/N-EXON OF THE HUMAN AND

; TITLE OF INVENTION: GENES

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSE: RECK, MAHN & CATE

; STREET: P.O. Box 06110

; CITY: CHICAGO

; STATE: ILLINOIS

; COUNTRY: U.S.A.

; ZIP: 60606-0110

; COMPUTER READABLE FORM:

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,962

; FILING DATE:

; CLASSIFICATION: 530

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/117,829

; FILING DATE: 08-SEPT-1993

; APPLICATION NUMBER: 07/721,571

; FILING DATE: 25-MAY-1990

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR89/00918

; FILING DATE: 25-JAN-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Fleit, Martin; Golian, Michael A.

; REGISTRATION NUMBER: 16,900; 31,957

; REFERENCE/DOCKET NUMBER: 47078-042

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 789-3400

; TELEFAX: (202) 789-1158

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 400 residues

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE:

; DESCRIPTION: Polypeptide

; US-08-450-962-6

Query Match Similarity 24.1%; Score 552.5; DB 4; Length 400;

Best Local Similarity 35.1%; Pred. No. 1.7e-34; Mismatches 141; Conservative 60; Indels 51; Gaps 15;

Matches 141; Conservatve 60; Mismatches 150; Indels 51; Gaps 15;

Qy 5 PGPPRANSTPA-WGAGP--PSAPGSG---WAAALCWVIAA-TAAANSLILALICIQ 54

Db 3 PWPHRHGSLLALWSAAPTDLPSAANNSGLCPVPAWAACALLATVGNNLIVTIAART 62

Qy 55 PALRRTSNEFLVLSLTDLMGLVYMPAMLNALYGRWLARGCLLWTAFDMCCSASI 114

Db 63 PRDQITNTNPFVTSAAADLVLGVGLVMPPGATLALTGHWPLGETCCELMWISDVICVTAI 122

Qy 115 LNLCLLISDRLYTLTISPLRYKLRLMPRLALALVIGAWSLAALASPLPLUGWHBLG--- 170

Db 123 ETLCALALAVDRYLAVTNPRLRYKLTYKRRARAAVVLWVVISSAASFAPIMSQWWRVGADAE 182

Qy 171 ---HARPPVPGOCRLASLPVFLVAVASGLFLFLSGATCPTCYCILLAARKQAVQASLT 236

Db 183 AQEHSNPRC---GSFASNMYALISSLSSVYFLPLVMLFYVAVFVVROR HLLRE 238

Qy 227 TGMASQASESLQVPRTPRP-----GVESADSR- RLATHSKRALKAKITLGILL 274

Db 239 LGRRSPPEESPPSPSRSPATGGTPAAPDGVPCCRPARLPLPREHRALR--TLGLIM 295

RESULT 8 ; Sequence 21, Application US/07626618A

; Patent No. 542265

; GENERAL INFORMATION:

; APPLICANT: Van Tol, Hubert H.M.

; TITLE OF INVENTION: A No. 542265el Human Dopamine Receptor and uses

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0. Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/626,618A

; FILING DATE: 7 DEC 1990

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 542265nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 90,1092

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 810-221-8317

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 446 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; US-07-626,618A-21

Query Match Similarity 24.1%; Score 552.5; DB 1; Length 446;

Best Local Similarity 31.2%; Pred: No. 1.9e-34; Mismatches 172; Indels 65; Gaps 13;

Matches 143; Conservatve 79; Mismatches 172; Indels 65; Gaps 13;

Qy 21 SAPGSGGW-----AAALCWVIAA-TAAANSLILALICQPAIRN-TSNFLFSI 68

Db 7 SAMDGTGLVERDEFSVRLTFLPSLFLSLLTFLGTLVCAVIRPFLKSKVNFVSL 66

Qy 69 FTSDLMGLVYMPAMLNALYGRWLARGCLLWTAFDMCCSASILNIGLISDRYLI 128

Db 67 AVSDLVAVIYVMPKAVAEAGFWPFG--SCNTIWFADINCMSTASINICVISDVRYWAI 125

Qy 129 LSPLRYKLRLMPRLALALVIGAWSLAALASPLPLUGWHBLGWHIGHARPPVG--- 178

Db 126 SSPFERYKTPKAFLISIYAVTLSIFQVOLSWHK--AKPTSFSDGNATSLAET 182

Qy 179 --QCLLASPLPVFLVAVASGLFLFLSGATCPTCYCILLAARKQAVQAVSI-TTGMAISOAE 235

Db 183 IDNCQSSLRHYATSSSVSYFVPAIMIVTYTRYRIQKOKRIMAAERAVAHAKNC 242

RESULT 9
 US-08-333-977-21
 Sequence 21, Application US/08333977
 Patent No. 5594108
 GENERAL INFORMATION:
 APPLICANT: Van Tol, Hubert H.M.
 ATTORNEY/AGENT: Civelli, Olivier
 PRIORITY APPLICATION DATA:
 TITLE OF INVENTION: A NO. 5594108el Human Dopamine Receptor and Uses
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Allegretti & Witcoff, Ltd.
 STREET: 10 South Wacker Drive, Suite 3000
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60605
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333, 977
 FILING DATE: 03-NOV-1994
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/626, 618
 FILING DATE: 7 DEC 1990
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5594108nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 90,1092
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 810-221-8317
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 US - 08-333-977-21

Query Match 24.1%; Score 552.5; DB 1; Length 446;
 Best Local Similarity 31.2%; Pred. No. 1.9e-34;
 Matches 143; Conservative 79; Mismatches 172; Indels 65; Gaps 13;

QY 21 SAGPGGSGW-----AAACWVIALTAANSLTALICTOPALRN-TSNNFLVSL 68
 ||| :||| | :||| | :||| | :||| | :||| | :||| | :||| | :||| |
 Db 7 SAMDGTTGLVERDEFSVRITACFLSLLSTLTLGNTLVCAAIRFRHLRSKVTFNFWLIS 66

QY 69 FWSDLMLVGLVWMPAMLNALYGVWLRGLCLWTAEDWMCSSAISLNCLISDRILL 128
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 10
 US-07-916-901-6
 Sequence 6, Application US/07916901
 Patent No. 5364772
 GENERAL INFORMATION:
 APPLICANT: Granneman, James G.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Lahmers, Kristine N.
 APPLICANT: Rao, Donald D.
 TITLE OF INVENTION: 6 @ 3 ADRENERGIC RECEPTOR PROTEIN AND DNA
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY S
 STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
 CITY: TROY
 STATE: Michigan
 COUNTRY: USA
 ZIP: 48099
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/916, 901
 FILING DATE: 19920720
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kohn, Kenneth I.
 REGISTRATION NUMBER: 30,955
 PRIORITY APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: P-324 (WSU)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (313) 689-3554
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 400 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-916-901-6

Query Match 24.1%; Score 551.5; DB 1; Length 400;
 Best Local Similarity 35.3%; Pred. No. 2e-34;
 Matches 142; Conservative 61; Mismatches 148; Indels 51; Gaps 15;

QY 5 PGPTANSTPA-WGAGP---PSAPGGSG----WVAALCVVIAL-TAAANSLTLALICTQ 54
 ; | | : | | || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 ; Db 3 PWPWKNGSLAFWSADAPTLDPSAANTSGLPGVPWAAAGALLALATVGGNLVTAIART 62
 QY 55 PALRNTSNEFLVLSLTSIDLAVGLVMPAMINALYGRWVLAARGCLLWTAFDVMCCSAST 114
 ; | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 ; Db 63 PRLOQTINNVFTSLATADLVGLVMPGATLALTGHWPLGATGCELMWTSVDVLCVTASI 122
 QY 115 LNLCCLSDRYLILSPRLYKLRMLPRLALVLGAWSLAALASPLPLLGWHELG--- 170
 ; | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 ; Db 123 ETLCALAVDRLYLAVINPLRGTLVTRRAAVVWIVSATVSEAPTSQWWRVGDAE 182
 QY 171 ---HARPPVPGQCRLLASLPFVLYASGLTFFLPSGAICTYCIRILLAARKOAVQVASLT 226
 ; | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 ; Db 183 AOECHSNPRC---CSFASNMPYALSSSVFYLPLVLMLEVARYFWVAKQR RLLRE 238
 QY 227 TGMASOASETLQVPRTPR-----GVESADSR - RLATHSKRALKAKLTGILL 274
 ; | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 ; Db 239 LGFPEPPEESPRSPRSRSPSPATVGTP-TASDQVSPSCRRPARLPLGEHRLR---TLGLIM 295
 QY 275 GMFVFTWLPLPVANTVQAVC - DCISPGFEDVLTWLGYCNSTMNPIY--PLMRDFKR 329
 ; | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 ; Db 296 GIEFSLCWLPFLANVLRAVGPSPVLTALNWLGYANSAFNPILYRSPDFAFR 355
 QY 330 AL---GRFLPCPRC---PREROASLASPLSR - TSHSGRP 362
 ; | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 ; Db 356 LICSYGGRGPFEEPRVTFPASPVASRQNSPLNRFDCYEGERP 397

RESULT 11
 US-07-783-602C-1
 ; Sequence 1, Application US/07783602C
 ; Patent No. 5418160
 ; GENERAL INFORMATION:
 ; APPLICANT: J. Craig Venter et al
 ; TITLE OF INVENTION: A FAT CELL SPECIFIC α -ADRENERGIC
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lowe, Price, LeBlanc & Becker
 ; STREET: Suite 300, 99 Canal Center Plaza
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: DOS Text File
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/783,602C
 ; FILING DATE: 19911101
 ; CLASSIFICATION: 436
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: J. G. Mullins
 ; REGISTRATION NUMBER: 33073
 ; REFERENCE/DOCKET NUMBER: 717-909
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703 684 1111
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 400
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Polypeptide
 ; US-07-783-602C-1

Query Match Local Similarity 24.1%; Score 551.5; DB 1; Length 400;
 Best Local Similarity 35.8%; Pred. No. 2e-34;

QY Matches 144; Conservative 61; Mismatches 146; Indels 51; Gaps 15;
 ; Sequence 1, Application US/08351473B
 ; Patent No. 5656440
 ; GENERAL INFORMATION:
 ; APPLICANT: LENZEN, GERLINDA
 ; APPLICANT: KAPOOR, ARCHANA
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ALEXINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/351,473B
 ; FILING DATE: 21-FEB-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 93 04670
 ; FILING DATE: 21-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR94/00447
 ; FILING DATE: 21-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-2220
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:

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